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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

US-09-252-991A-3017/c Sequence 3017, Application US/0925291A Patent No. 6551795 GENERAL INPORMATION: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US 60/074,788 PRIOR PLING DATE: 1998-02-18 PRIOR PLING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 3017 TYPE: DNA TYPE: DNA	/ Ordanism: Sendomonas aeruginosa // Ordanism: Sendomonas aeruginosa // Oscore 20; DB 4; Length 249; Dest Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1920 GGAGACCGCATGACCTTCG 1939 Db 108 GGAGACCGGCATGACCTTCG 89	RESULT 2 US-09-313-294A-7021/C i Sequence 7021, Application US/09313294A i Patent No. 6476212 i BENERAL INFORMATION: APPLICANT: Lalgudi, Raghunath V. APPLICANT: Lalgudi, Raghunath V. APPLICANT: Ito, Laura Y. APPLICANT: Sherman, Paradley K. TILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US CURRENT APPLICATION NUMBER: US/09/313,294A CURRENT FILING DATE: 1999-05-14 NUMBER OF SEQ ID NOS: 7600 SOFTWARE: PERL Program SEQ ID NO 7021 ILENGTH: 311 TYPE: DNA ORGANISM: Zea mays
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Sequence 2651, Application US/0925291A
Sequence 2651, Application US/0925291A
Sequence 2651, Application US/0925291A
Sequence 2651, Application US/0925291A
Sequence 2651, Application
Sequence 2651, Application
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRERENCE: 107196.136
CURRENT BILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
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APPLICANT:
APPLICANT:
MARC J. RUBEHFIELD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: APRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS.
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
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; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           687 GGAGACCGCATGACCTTCG 706
                                        ; NAME/KEY: misc_feature
; LOCATION: (1)...(616)
; CTHER INFORMATION: n = A,T,C or G
US-09-385-982-238
                                                                                                                                                                                                                                                                                                                                                                                                            71 CAACTCCACCGTCTCCAGGA 52
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-252-991A-2651
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Patent No. 662933

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Application USPICANT: Applicant: Madeline Joy
APPLICANT: Mangy Tongtong
APPLICANT: Benson, 120121.47102
APPLICANT: Benson, 120121.47102
APPLICANT: Benson, 120121.47102
APPLICANT: APPLICATION NUMBER: US/09/401,064
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 371
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 165
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4

US-09-385-982-238/C

Sequence 238, Application US/09385982

Patent No. 6262334

GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
ITILE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
ITILE OF INVENTION: PRODUCTS: II
FILE REPERANCE: CCDNA_260XX

CURRENT APPLICATION NUMBER: US/09/385,982

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: 60/17,393

EARLIER PILING DATE: 1999-06-08

FRALIER PILING DATE: 1998-08-31

NUMBER: OF SEQ ID NOS: 544

SOFTWARE: PRESEQ FOR WINDOWS VERSION 3.0

SEQ ID NO 280 ID NOS: PRESEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.4%; Score 20; DB 4; Length 462; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        Query Match

0.4%; Score 20; DB 4; Length 311;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels
) NAME/KEY: misc feature

) OTHER INFORMATION: Incyte ID No. 6476212 700381005H1

) NAME/KEY: unsure

) OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-7021
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ORGANISM: Homo sapien
US-09-401-064-165
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Gaps

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0; Indels

DB 4; Length 1029; 14;

Query Match 0.4%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches

1920 GGAGACCGGCATGACCTTCG 1939

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TYPE: DNA ORGANISM: Homo sapiens

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APPLICANT: SPARKS, Andrew B.
APPLICANT: WORDWAY, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLKES, Dana M.
APPLICANT: FOWLONELL, Stephen J.
ITLE OF INVENTION: POLYPEPTIONS HAVING A FUNCTIONAL
TITLE OF INVENTION: USING SAME
TITLE OF INVENTION: USING SAME
CORRESPONDENCE: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036-271
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: DEFENTIN RELEASE #1.0, Version #1.30
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLING DATE: 03-APR-1996
CLASSIFICATION: 356
ATTORNEY/AGBNT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 10.974
TELEPHONE: (212) 869-8864/9741
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-8864/9741
SEQUENCE CHRARACTERISTICS:
SEQUENCE CHRARACTERISTICS:
TENGRALIN FOR SEQ ID NO: 31:
SEQUENCE CHRARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.4%; Score 20; DB 4; Best Local Similarity 100.0%; Pred. No. 15; Matches 20; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-620-312D-702/c
; Sequence 702, Application US/09620312D
; Patent No. 6569662
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1, Application US/08630915A
6309820
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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aldong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Mang, Yunging
Mang, Dunrui
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LENGTH: 1636 Dac.
TYPE: nucleic acid
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US-09-976-594-779/C
Sequence 779, Application US/09976594
Fatent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness Michael
APPLICANT: Furness Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT PLING DATE: 2001-10-12
FRIOR PAPPLICATION NUMBER: 60/240,409
FRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SEQ ID NO 779
LENGTH: 1456
                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%; Score 20; DB 4; Length 1455; 100.0%; Pred. No. 15; tive 0; Mismatches 0; Indels
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CTHER INFORMATION: Incyte ID No. 6673549 1384716.4
NAME/KEY: unsure
LOCATION: 1453
CTHER INFORMATION: a, t, c, g, or other
US-09-976-594-779
                                                                                                                                       US-09-252-991A-3212/c
; Sequence 3212, Application US/09252991A
; Patent No. 6551795
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                    361 GGAGACCGGCATGACCTTCG 380
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CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-3212
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Best Local Similarity 100.0
Matches 20, Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-08-630-915A-31
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Sequence 1, Application US/09141908
Patent No. 6503741
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SHIEK, GENY
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/09320878A
| Sequence 19, Application US/09320878A
| Patent No. 6117659
| GENERAL INFORMATION:
| APPLICANT: BETLACH, Mary C. APPLICANT: BETLACH, Mary C. APPLICANT: BETLACH, Mary C. APPLICANT: TANG, Li
| TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 300622012120
| CURRENT APPLICATION NUMBER: US/09/320,878A
| CURRENT PILING DATE: 1999-05-27
| CURRENT APPLICATION NUMBER: CIP OF 09/141,908
| EARLIER FILING DATE: 1998-08-28
| EARLIER APPLICATION NUMBER: CIP OF 08/846,247
| EARLIER PILING DATE: 1999-02-08
| EARLIER PILING DATE: 1999-02-08
| EARLIER PILING DATE: 1998-06-28
| EARLIER APPLICATION NUMBER: G0/119,139
| EARLIER PILING DATE: 1998-06-08
| EARLIER PILING DATE: 1998-06-08
| EARLIER PILING DATE: 1998-06-28
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17;
                                                                                                                                                                                                                                                                   Length 36778;
                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                Query Match 0.4%; Score 20; DB 3; Best Local Similarity 100.0%; Pred. No. 17; Matches 20; Conservative 0; Mismatches C
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 36778
TYPE: DAA
TYPE: DAA
US-09-105-537-5
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; ORGANISM: Streptomyces venezuelae
US-09-320-878-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 38506
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US-09-320-878-19/c
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US-09-141-908-1/c
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US-09-105-537-30/c

Sequence 30, Application US/09105537A

Patent No. 626502

GENERAL INFORMATION:

APPLICANT: Sherman, D.H.

APPLICANT: Liu, H.

APPLICANT: Liu, Y.

APPLICANT: Liu, Y.

APPLICANT: APPLICANT: Co. 0.438US1

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT APPLICATION NUMBER: US/09/105,537A

CURRENT PILING DATE: 1998-06-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 30

LENGTH: 13842

TYPE: DNA

CORGANISM: Streptomyces venezuelae

US-09-105-537-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.4%; Score 20; DB 3; Length 13842; Best Local Similarity 100.0%; Pred. No. 16; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 4; Length 2522;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
  APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 784CIP2B
CURRENT PILING DATE: 2000-07-19
FRICH APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
FRICH APPLICATION NUMBER: 09/552,317
FRICH FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO SEQ ID NOS: 1105
SEQ ID NO SEQ ID NOS: 1105
LENGTH: 2522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 15; Matches 20; Conservative 0; Mismatches
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US-09-105-537-5/C
US-09-105-537-5/C
Sequence 5, Application US/09105537A
Parent No. 6265202
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Xue, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10196 AACTCCACCGTCTCCAGGAC 10177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (179)..(1606)
US-09-620-312D-702
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Zhao, L. TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1

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Page 5
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| Sequence | 19, Application US/09657440 |
| Parent No. 6509455 |
| GENERAL INFORMATION |
| APPLICANT | ASFLEX, Gary | | |
| APPLICANT | BETLACH, Melanie C. |
| APPLICANT | BETLACH, Melanie C. |
| APPLICANT | BETLACH, Melanie C. |
| APPLICANT | APPLICANT | ACOMBINAT | APPLICANT |
| APPLICANT | TANG, Li |
| TITLE OF INTORNION RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE |
| TITLE OF INTORNION RECOMBINANT | 1000 |
| TILLE OF INTORNION NUMBER: US/09/657,440 |
| CURRENT FILING DATE: 1999-05-27 |
| PRIOR PLILING DATE: 1999-05-27 |
| PRIOR PLILING DATE: 1999-05-27 |
| PRIOR PLILING DATE: 1998-08-28 |
| NUMBER OF SEQ ID NOS: 34 |
| SOFTWARE: Patentin Ver. 2.0 |
| LENGTH: 38506 |
| MUNDER OF SEQ ID NO 19 |
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0.4%; Score 20; DB 4; Length 38506;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0
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0.4%; Score 20; DB 4; Length 38506;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
FILE REFERENCE: 300622002100
CURRENT APPLICATION NUMBER: US/09/141,908
CURRENT FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER PILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
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Search completed: May 23, 2004, 12:40:27 Job time : 265 secs us-09-964-956-12.rnpb

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May 23, 2004, 11:35:39 ; Search time 1466 Seconds (without alignments) 17642.596 Million cell updates/sec
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1. \(\cgn2_6\)\prodata/2\pubpna/USO7 \(\text{PUBCOMB.seq:*}\)

2. \(\cgn2_6\)\prodata/2\pubpna/USO7 \(\text{PUBCOMB.seq:*}\)

3. \(\cgn2_6\)\prodata/2\pubpna/USO7 \(\text{BW}\)\Pub.seq:*

4. \(\cgn2_6\)\prodata/2\pubpna/USO6\)\PubBCOMB.seq:*

5. \(\cgn2_6\)\prodata/2\pubpna/USO6\)\PubBCOMB.seq:*

6. \(\cgn2_6\)\prodata/2\pubpna/USO8\)\PubPUB\\PubBCOMB.seq:*

7. \(\cgn2_6\)\prodata/2\pubpna/USO8\)\PubPUB\\PubBCOMB.seq:*

8. \(\cgn2_6\)\prodata/2\pubpna/USO8\)\PubPUB\\PubBCOMB.seq:*

9. \(\cgn2_6\)\prodata/2\pubpna/USO9\PubPUB\PubBCOMB.seq:*

10. \(\cgn2_6\)\prodata/2\pubpna/USO9\PubBCOMB.seq:*

11. \(\cgn2_6\)\prodata/2\pubpna/USO9\PubB\PubBCOMB.seq:*

12. \(\cgn2_6\)\prodata/2\pubpna/USO9\PubB\PubBCOMB.seq:*

13. \(\cgn2_6\)\prodata/2\pubpna/USO9\PubB\PubBCOMB.seq:*

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18. \(\cgn2_6\)\prodata/2\pubpna/USO0\PubBCOMB.seq:*

19. \(\cgn2_6\)\prodata/2\pubpna/USO0\PubBCOMB.seq:*

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19. \(\cgn2_6\)\prodata/2\pubpna/USO0\PubBCOMB.seq:*

19. \(\cgn2_6\)\prodata/2\pubpna/USO0\PubBCOMB.seq:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

,	Appl	Appl		Appl	App1									
	12,	19,	802,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence
ΠD	US-09-964-956-12	US-10-451-010-19	US-10-108-260A-802	US-10-245-752-91	US-10-245-859-91	US-10-245-103-91	US-10-245-107-91	US-10-245-143-91	US-10-245-771-91	US-10-245-851-91	US-10-245-883-91	US-10-237-535-91	US-10-238-183-91	US-10-238-283-91
DB	13	17	16	13	13	15	15	15	15	15	15	15	15	72
% Query Match Length D	5691	6367	3666	2597	2597	2597	2597	2597	2597	2597	2597	2597	2597	2597
% Query Match	100.0	97.2	19.5	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.9
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5 US-10-238-370-91	-10-245-	US-10-245-147-	US-10-245-	US-10-245-739-	US-10-246-210-	US-10-239-196	US-10-243-024-	US-10-243-409	US-10-245-	US-10-245-88	US-10-245-	US-10-243-095-	US-10-245-	US-10-245-427-	US-10-245-473-	US-10-24	US-10-245-877	US-10-246-976-	US-10-243-320	US-10-242-743-	US-10-242-84	US-10-237-636	US-10-238-325-	US-10-238-346-	US-10-238-411-	US-10-243-124-	US-10-243-425	US-10-243-446	US-10-245-874	US-10-242-653-
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ALIGNMENTS

```
GENERAL INFORMATION:

APPLICANT: Gerlach, Valerie L
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Grose, Milliam M
APPLICANT: Grose Milliam M
APPLICANT: Lepley, Denise M
APPLICANT: Lepley, Denise M
APPLICANT: Depley, Denise M
APPLICANT: Stone, Marchine E
APPLICANT: Rekuda, Ramesh
APPLICANT: Stone, Martin D
APPLICANT: Stone, Minbern GO/235, 631
PRIOR APPLICATION NUMBER: GO/235, 632
PRIOR APPLICATION NUMBER: GO/235, 608
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: GO/236, 664
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: GO/236, 665
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: GO/236, 665
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: GO/236, 665
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: GO/236, 665
PRIOR APPLICATION NUMBER: GO/236, 666
RESULT 1
US-09-964-956-12
'Sequence 12, Application US/09964956
'Publication No. US20040043926A1
'GENERAL INFORMATION:
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  GAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCCTGACTTT
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5691; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-26
PRIOR PELLING NUMBER: 60/237,434
PRIOR PELLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-05
PRIOR PELLING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2000-10-06
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
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PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-05-31
PRIOR PILING DATE: 2001-07-31
                                                                                                                                                                     ) LENGTH: 5691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-956-12
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            GATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTTTGTCTACTTTTTGACCCTCCAA
                                                                                                                                              CCTGAGATGGTGTCTCCACCAGGCTCCACCAAGGAGCAGGTGTATACATCCAAGGTC
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FILE REFERENCE: PF-0867 USN
CURRENT APPLICATION NUMBER: US/10/451,010
CURRENT FILING DATE: 2003-06-17
PRIOR APPLICATION NUMBER: PCT/US01/49206
PRIOR PELING DATE: 2001-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-05
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2000-12-20
PRIOR PELING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL PROGram
SEQ ID NO 19
LENGTH: 6367
TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID NO: 7156379CB1
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NAME/KEY: unsure
LOCATION: 166
US-10-451-010-19
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OV 5041 CTCTGGCGCTAAGGGCACTGCAGAAGTTTGTGGATGACCTGTTTGAGACCATCTTC 5100	5606 CTCCTGGCCACTAAGGGCACACTGCAGAAGTTTGTGGATGACCTCTTTGAGACCATCTTC	Db 5161 AGAGGGCACACGGGGCCTGCCCTGGCCTGGCCAGGATACATGTTTGCTG 5180 S666 AGAGGGCACACGTGGCTTGCCTGCCCTGGCCATGCAGGATACATGTTTGCTG 5725 Qy 5161 GATGAGGGCTGATAAACATGGCATTCATGACGGCGCGCGC	5726 GATGAGCAGGCTGATAAACATGGCATTCATGACCCGCACGTCCGCCATACCTGGAAAGAGC 5221 AATTGCCTGCCCCTGAGGTTTTGGGTCAACATGAACAACCCGCAGTTTGTGTTTTGAC	Db 5786 AATTGCCTGCCCTGAGGTTTTGGGTCAACATGATCAAGAACCCGCAGTTTGTGTTTTGAC 5845 Qy 5281 ATCCATAAGAACAGCATCACAGACGCCTGCCTCTCTGTGGTGGTCAGACCTTCATGAC 5340 Db 5846 ATCCATAAGAACAGCATCAAGAACGCCTGCCTCTCTGTGGTGGTGAGCTTCATGGAC 5905	5341 TCTTGCTCCACGTCAGAGCACCGGCTGGCCAGGACGCCTCCAACAAGCTGCTGTAT		AGCAGTCCCGGATGCAC 5	aaatac aaatac	TGGGAAGC TGGGAAGC	Oy 5641 TACAACTGGAACAAGTCATAACCTCATGGACAGCTGA 5685	RESULT 3 US-10-108-260A-802 ; Sequence 802, Application US/10108260A		CURRENT APPLICATION NUMBER: US/10/108,260A CURRENT FILING DATE: 2002-03-27 CURRENT FILING DATE: 2005-6458 CURRENT PILING DATE: 2002-03-27	01	-802 19.5%;	Best Local Similarity 99.9%; Pred. No. 0; Matches 1158; Conservative 0; Mismatches 1; Indels 0; Gaps 0	1 TOTORS OF THE PROPERTY OF TH
4466 CATGAGCTGACCAGTGACCTGGATGGAGCCGGGATTCCGTTCCTGGACTATAGAACTTAC 4525	3961 ACCATGCGGGTGCTGTTCCCAGGAATTGAAGACCACCCTGTCCTCCGGGACCTTGAGGTC 4020	CCGGGCTACCGGCAGGAGCGTGGAGAAAGGCCTGAAGCTCTTCGCCCAGCTCATCAAC 408	4081 AACAAGTIGTTCCTGCTGTCCTTCATCCGCAGGCTTGAGTCCCAGGGTAGGTTCTCCATG 4140	CGGGACGAGGGCAACGAGGGCCTCACTGATGACCGTGCTGCAGAGGAAGAGCAAGGCTGGAAGTACGGCACGACGAGGAAGTACGACGACGACGACGACCTCATTGACAAGAACCTGGAAGAAGAACTGGAAGAAGAACTGGAAGAACCTGGAAGAACTGAAAGAACTAGAAAAGAACTACTGAAAACAACTACTAGAAAGAA	AACCACCTAAGCTGCTGCTGAGAGGACTGAGTCAGTGGCTGAAAAGAGATGCTGACCAAT 432 	4321 TGGTTTACTTTCCTCTTACAAGTTCCTCAAGGAGTGTGCTGGGGAGCCCCTCTTCTCC 4380	4381 CTGTTCTGTGCCATCAAGCAGCAGAAGGGCCCCATTGACGCCATCACGGGGGAG 4440	GCCGGTACTCCTTGAGCGAGGACAAGCTCATCCGCCAGCAGATTGACTACAAAACCCTG	4501 GTCCTGAGCTGTCTCAGCCCAGACAATGCCAACAGCCCCGGAGGTCCCAGTAAAGATCCTC 4560	4561 AACTGTGACACCATCACTCAGGTCAAGGAGAAGATTCTGGATGCCATCTTCAAGAATGTG 4620 	4621 CCTTGCTCCCACCGGCCCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGG 4680	4681 GCAAGGATGATCTTGCAGGATGAAGACATCACCACCAAGATTGAGAATGGAATGGAAGGGA 4740 	4741 CTGAACACACAGCCCACTACCAGGTGCCAGATGGTTCCGTGGTGGCATTAGTGTCCAAG 4800	4801 CAGGIGACAGCCTATAACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAAA 4860 	4861 TATGAAAACATGATCGGGTACACGGGCAGCCCGGACGCTCGGCTCAGGACACCTATG 4920	4921 ATCACTCCTGACCTGGAGOTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCAC 4980	とこととことに、このように、 GGLGLGGLGLGLGLLLLOLOLLLLLLLLLLLLLLLLLL

Db 1141 CATGAGCTTAGACAGCTGA 1159	RESULT 4 US-10-245-752-91 Sequence 91, Application US/10245752 Publication No Resonance 4231	GENERAL INFORMATION: APPLICANT: Baker, Kevin APPLICANT: Bater, Kevin APPLICANT: Bilan		# APPLICANT: Stephan Jean-Phillippe # APPLICANT: Watanbe, Colin # APPLICANT: Watanbe, Colin # APPLICANT: Wood, William # APPLICANT: Stephan Jean	# AFPLICAN1: Intelly.Centure ### APPLICAN1: Fong.Sherman ### TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC #### TITLE OF INVENTION: ACIDS ENCODING THE SAME #### APPLICAN1: PAGE PROPERTY THE SAME	; FILE REFERENCE: PS-30RLCse ; CURRENT APPLICATION NUMBER: US/10/245,752 ; CURRENT FILING DATE: 2002-09-16 ; PRIOR APPLICATION NUMBER: 10/197942	FRIOR APPLICATION NUMBER: 60/05914 PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/063046) PRIOR APPLICATION NUMBER: 60/065027) PRIOR PILING DATE: 1997-11-10) PRIOR FILING DATE: 1997-11-10) PRIOR APPLICATION NUMBER: 60/079689	FRIOR APPLICATION NUMBER: 60/086478 ; FRIOR FILING DATE: 1998-05-22 ; FRIOR FILING TOWNER: 60/087607	; PRIOR APPLICATION NUMBER: 60/098801 ; PRIOR FILING DATE: 1998-06-18 ; PRIOR FILING DATE: 00/090557	FALOR FILING DATE: 1998-06-24; PRIOR APPLICATION UNMERS: 60(09689) PRIOR FILING DATE: 1998-06-25 Remaining Prior Application data removed - See File Wrapper or PALM.		nomo sapien 91 13.9%; Score 793;	o; Misu	Db 1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 60	69 CHICACCARCATCCTGARGACTTGARGACTTGARGACTTGARGATTAAGATCCCTTCGAGACAC	121	181 TGTCTACTTTTGACCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCAAGGA
Db 61 GGAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCACGGCCCAAAGCTGC 120	4647 AGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGA 4706 	4707 CATCACCACCAAGATTGAGAATGATTGGAAGGGACTGAACACACTGGCCCACTACCAGGT 4766	4767 GCCAGATGCTTCCGTGGTGGCATTAGTGTCCCAAGCAGGTGACAGCCTATAACGCAGTGAA 4826 	4827 CBACTCCACCGTCTCCAGGACTCAGCAGTBAATATGAAAACATGATCCGGTACACGGG 4886	4887 CAGCCCCGACAGCTCCGCTCACGGACACCTATGATCACTCCTGACCTGGAGAGAGGGGGT 4946	4947 CAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGGCCGGGG 5006	5007 GAGCAAGATGGTGTCTGAAATCTACCTGACCCGACTCGTGGCCACTAAGGGCACACTGCA 5066 481 GAGCAAGATGTCTGAAATCTACCTGACCCGACTCGTGGCCACTAAGGGCACACTGCA 540	5067 GAAGTTTGTGGATGACCTCTTTGAGACCATCTTCAGCACGGGACGCGTGGCTCTGCCT 5126	5127 GCCCTGGCCATCAAGTACATGTTTGACTTCCTGGATGAGCAGGCTGATAAACATGGCAT 5186	5187 TCATGACCCGCACGTCCGCCATACCTGGAAGAGCAATTGCCTGCC	5247 CAACATGATCAAGAACCCGCAGTTTGTGTTTGACATCCATAAGAACAGCATCACAGACGC 5306	5307 CTGCCTCTCTGTGGTCGGTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCACCGGCT 5366	5367 GGGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCAGCTACAAGAA 5426 	5427 TIGGGIGGAGAGGTATTACTCAGACATAGGGAAGAIGCCAGCCATCAGCGACCAAGACAT 5486 	5487 GAACGCATACCTGGCTGACGCTCCCGGATGCACATGAATGA	SANCELEARING LEGGLEGAGGER GEGRACATEGAGGER LEAGACATEGAGGER ACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGGGGAGAGATCCTTGGAACCTCTGGAACATCTCTGGAACATTCTCTGAAATAACAGAGAATCTTCTTGAATAATAACAGAGAATACTTCAGAAATAACATGAAAAAAAA	CCACGATGACCASTGTGGGAAGGAGAACTGGCCTACAACTAGAACAGTCATAACCCT CCACGACGACGACGAAGGAGAAACTGGCCTACAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTGAAACTAAAACTGAAAACTAAAACTAAAACTAAAACTAAAACTAAAACTGAAAACTGAAAACTGAAAACTAAAACTGAAAACTGAAAAACTAAAACTAAAAAAAA	CATGAGCTTAGACAGCTGA 5685

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PRIOR APPLICATION NUMBER: 60/086478
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PRIOR APPLICATION NUMBER: 60/089801
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See Fill
SEQ ID NO 91
LENGTH: 2597
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13.9%; Score 793; DE
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches
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CORGANISM: Homo Sapien
US-10-245-859-91
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APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Goddard, Auderin
APPLICANT: Goddard, Auderin
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Sherman
APPLICANT: Sherman
APPLICANT: And Augerin
APPLICANT: AND ARENCE STEPHAN AUGURE
APPLICANT: AND AUGURE
APPLICANT: AUGURE
APPLICANTON NUMBER: U) 197942
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-10-24
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Sequence 91, Application US/10245107
Sequence 91, Application US/10245107
Publication No. US2030068779A1
GENERAL INFORMATION:
APPLICANT: Eaker.Kevin
APPLICANT: Eaker.Man
APPLICANT: Application Audien
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Sephan, Jean-Phillippe
APPLICANT: Sephan, Jean-Phillippe
APPLICANT: Scanha, Jean-Phillippe
APPLICANT: Scanha, Jean-Phillippe
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Mod, William
APPLICANT: Mod, William
APPLICANT: Mod, William
APPLICANT: ADAIS SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
FILE REFERENCE: P3501RC71
CURRENT APPLICATION NUMBER: US/10/7942
PRIOR APPLICATION NUMBER: US/10/7942
PRIOR PLLING DATE: 2002-07-18
PRIOR PLLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/653046
PRIOR APPLICATION NUMBER: 60/653046
PRIOR APPLICATION NUMBER: 60/65027
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Sequence 91, Application US/10245103

Sequence 92, Application US/10245103

Sequence 92, Application WS- US2030068778A1

APPLICANT: Baker.Kevin

APPLICANT: Grimaldi, 7. Christopher

APPLICANT: Grimaldig Pricor Application data removed - See File Wrapper or PALM.

TUPP: No. 91

LEMSTRIA SPA
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13.9%; Score 793; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches
.359 CAAGCTGAAGAAG 1371
|||||||||||||
781 CAAGCTGAAGAAG 793
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; ORGANISM: Homo Sapien
US-10-245-103-91
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CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 758
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                                                                                                                               1359 CAAGCTGAAGAAG 1371
                                                                                                                                                                               781 CAAGCTGAAGAAG 793
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; ORGANISM: Homo Sapien
US-10-245-143-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 TIGITACCGGGGCGACGACCTGGACCTGGCCTGGCTCAAGGTGAAGGTCCCCTG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 638
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PRIOR APPLICATION NUMBER: 60/079689

PRIOR PLILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/086478

PRIOR FILING DATE: 1998-05-22

PRIOR PELING DATE: 1998-05-22

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

PRIOR FILING DATE: 1998-06-18

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PRIOR FILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-24

PRIOR PILING DATE: 1998-06-24

PRIOR PILING DATE: 1998-06-25

NOWBER OF SEQ ID NOS: 116

SEQ ID NO 91

LENGTH: 2597

**CHARLING DATE: 1998-06-25

**CHARLING DATE: 1998-06-26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             699 CTTCACCATCATCCTGACTTTGATATCTACTATGTCTATGGTTTTAGGAGTGGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          759 TGICIACITITICACCCICCAACCIGAGAIGGIGICICCACCAGGCICCACCACCAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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13.9%; Score 793; DB 15; Length 2597;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0
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; ORGANISM: Homo Sapien
US-10-245-107-91
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1299 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACAAAAGTGG 1358
        721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCGCCTTTGTGGGCACCAAAAGTGG 780
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TIGITACCGGGGCGAGGCACGCTGGACCTGGCCTGAGGTGAAGGAGACATCCCCTG 1178
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PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-11-60/065027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR APPLICATION NUMBER: 60/090557
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-18
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PRIOR PILING DATE: 1998-06-18
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo Sapien
US-10-245-771-91
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US-10-245-771-91

Sequence 91, Application US/10245771

Publication No. US20030068781A1

Publication No. US20030068781A1

APPLICANT: Baker, Kevin

APPLICANT: Eaton, Dan

APPLICANT: Goddard, Addrey

APPLICANT: Girlandid, J. Cirristopher

APPLICANT: Sitch, Victoria

APPLICANT: Sitch, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Adaption

APPLICANT: Abang, Zemin

APPLICANT: Adaption

APPLICAN
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APPLICANT: SILTEN, VARIETA
APPLICANT: SILTEN, VACCOTA
APPLICANT: SILTEN, VACCOTA
APPLICANT: SILTEN, VACCOTA
APPLICANT: MATADBC ANILLIAN
APPLICANT: PORGAS SHERMAN
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION WINDER: 10/19942
PRIOR FILING DATE: 1997-10-11
PRIOR PRIOR FILING DATE: 1997-10-11
PRIOR PRIOR FILING DATE: 1997-10-12
PRIOR FILING DATE: 1998-10-12
PRIOR FILING DATE: 1998-10-12
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-07-07
PRIOR PAPLICATION NUMBER: 60/10055
PRIOR PAPLICATION NUMBER: 60/10053
PRIOR PAPLICATIO
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T. Gormaldi, J. Christopher
TT. Gurney, Austin
TT. Smith, Victoria
TT. Stephan, Jean Phillippe
TT. Watanbe, Colin
TT. Wood, William
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Publication No. US20030073188A1
APPLICANT: Baker, Kevin
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100.0%; Pred. No. 0;
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Best Local Similarity 100.
Matches 793; Conservative
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CORGANISM: Homo Sapien
US-10-245-883-91
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R FILING DATE: 1999-12-09
R APPLICATION NUMBER: 60/177118
R PILING DATE: 2000-01-20
R APPLICATION NUMBER: 60/179118
R FILING DATE: 2000-02-02
R APPLICATION NUMBER: 60/18921
R FILING DATE: 2000-02-08
R APPLICATION NUMBER: 60/187202
R APPLICATION NUMBER: 60/187202
R APPLICATION NUMBER: 60/19618
R FILING DATE: 2000-03-03
R FILING DATE: 2000-04-18
R FILING DATE: 2000-04-18
R FILING DATE: 2000-04-18
R FILING DATE: 2000-04-25
R APPLICATION NUMBER: 60/19614 R FILING DATE: 2000-05-23

R APPLICATION NUMBER: 60/206368

R APPLICATION NUMBER: 60/20932

R APPLICATION NUMBER: 60/20932

R PILING DATE: 2000-06-05

R PILING DATE: 2000-06-05

R FILING DATE: 2000-07-13 APPLICATION NUMBER: 60/144790
APPLICATION NUMBER: 60/144790
PILING DATE: 1999-07-20
APPLICATION NUMBER: 60/14528
FILING DATE: 1999-07-20
APPLICATION NUMBER: 60/14528
FILING DATE: 1999-07-26
APPLICATION NUMBER: 60/14622
APPLICATION NUMBER: 60/14622
FILING DATE: 1999-07-28
APPLICATION NUMBER: 60/14683
FILING DATE: 1999-08-10
APPLICATION NUMBER: 60/14818
FILING DATE: 1999-08-10
APPLICATION NUMBER: 60/14818
FILING DATE: 1999-08-10
APPLICATION NUMBER: 60/14853
FILING DATE: 1999-08-10
APPLICATION NUMBER: 60/14853
FILING DATE: 1999-08-17
FILING DATE: 1999-08-17
FILING DATE: 1999-08-17 R APPLICATION NUMBER: 60/149395
R FILING DATE: 1999-08-17
R FILING DATE: 1999-08-20
R APPLICATION NUMBER: 60/151700
R APPLICATION NUMBER: 60/151700
R APPLICATION NUMBER: 60/151734
R PILING DATE: 1999-08-31 R FILING DATE: 1999-04-27
R APPLICATION NUMBER: 60/133459
R FILING DATE: 1999-05-11
R PRILING DATE: 1999-05-25
R RILING DATE: 1999-05-25
R APPLICATION NUMBER: 60/135729 APPLICATION NUMBER: 60/222695 FILING DATE: 2000-08-02 PPLICATION NUMBER: 60/162506 ILING DATE: 1999-10-29 PPLICATION NUMBER: 60/170262 APPLICATION NUMBER: 60/229896 LING DATE: 1999-05-25
PPLICATION NUMBER: 60/135750
ILING DATE: 1999-06-25
FULCATION NUMBER: 60/138385
ILING DATE: 1999-06-09 APPLICATION NUMBER: 60/141037 FILING DATE: 1999-06-23 APPLICATION NUMBER: 60/144732 LING DATE: 1999-07-20 PLICATION NUMBER: 60/144758 LING DATE: 1999-06-09 PLICATION NUMBER: 60/140653 G DATE: 1999-04-01 CATION NUMBER: 60/131271 1999-07-20 LING DATE: 1999-06-2 PRIOR PRIOR

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PRIOR FILING DATE: 2000-09-05
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PRIOR PLING DATE: 1009-03-19
PRIOR PLING DATE: 1009-03-19
PRIOR PLING DATE: 2001-03-9
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Length 2597;

DB 15;

Score 793;

13.9%;

Query Match

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APPLICATION NUMBER: 60/145228
FILING DATE: 1999-07-20
APPLICATION NUMBER: 60/145698
FILING DATE: 1999-07-26
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                    0; Indels
Best Local Similarity 100.0%; Pred. No. 0; Matches 793; Conservative 0; Mismatches
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US-02-238-183-91
US-02-238-183-91
US-02-238-183-91
Sequence 91, Application US/10238183
Publication No. US20030073189A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Godard, Audrey
APPLICANT: Godard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
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RETITING DATE: 1999-08-31

RAPPLICATION NUMBER: 60/162506

RAPPLICATION NUMBER: 60/170262

RETLING DATE: 1999-12-09

RETLING DATE: 1999-12-09

RETLING DATE: 1999-12-09

RETLING DATE: 2000-01-20

RETLING DATE: 2000-02-02

RETLING DATE: 2000-02-02

RETLING DATE: 2000-02-02

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RETLING DATE: 2001-01-16

RETLING DATE: 2001-01-18

RETLING DATE: 2001-01-01-18

RETLING DATE: 2001-01-01-01-R APPLICATION NUMBER: 60/146222
R FILING DATE: 1999-07-28
R APPLICATION NUMBER: 60/146843
R FILING DATE: 1999-08-03
R FILING DATE: 1999-08-03
R FILING DATE: 1999-08-10
R APPLICATION NUMBER: 60/148513
R APPLICATION NUMBER: 60/148513
R APPLICATION NUMBER: 60/149527
R APPLICATION NUMBER: 60/149327 R FILING DATE: 1999-08-17
R RAPLICATION NUMBER: 60/149395
R PILING DATE: 1999-08-17
R APPLICATION NUMBER: 60/150114
R PILING DATE: 1999-08-20
R APPLICATION NUMBER: 60/151700 APPLICATION NUMBER: 60/151734 FILING DATE: 2001-04-04 APPLICATION NUMBER: 60/282199

61 GITCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120 181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCCACCAGGCTCCACCACGAGGA 240 301 IGTAGAGGTGCCCATTGGCTGTGGCGCAGTGGGGTGGGGGGTACCGCCTGCTGCAGGTGC 360 121 CTTCACCATCATCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180 759 IGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCAAGGA 818 241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACACAGGCTTCAACTCCTA 300 879 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938 639 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 819 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACACCCTTCAACTCCTA Gaps CTTCACCATCATCCTGACTTTGATATCTACTATGTCTATGGTTTTTAGCAGTGGCAACTT ö Query Match 13.9%; Score 793; DB 15; Length 2597; Best Local Similarity 100.0%; Pred. No. 0; Matches 793; Conservative 0; Mismatches 0; Indels 0 669 н PRIOR
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PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 91
LENGTH: 2597
                                                              TYPE: DNA
CORGANISM: Homo Sapien
US-10-238-283-91
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Best Local Similarity
Matches 793; Conserv
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13.9%; Score 793; DB 15; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0;

Length 2597;

US-10-238-283-91
| Sequence 91, Application US/10238283
| Sequence 91, Application US/10238283
| Publication No. USZO030073190A1
| GENERAL INFORMATION:
| APPLICANT: Baker.Kevin
| APPLICANT: Baker.Kevin
| APPLICANT: Baker.Kevin
| APPLICANT: Selven.Dan
| APPLICANT: Watanbe.Colin
| APPLICANT: Watanbe.Colin
| APPLICANT: Selven.Dan
| APPLICANT: Selven.Dan
| APPLICANT: Selven.Dan
| APPLICANT: Batanbe.Colin
| APPLICANT: Polg.Selven.Dan
| PRIOR FILING DATE: 1998-06-10
| PRIOR PLING DATE: 1998-06-10

1238 1358 1178 1058 540 720 480 600 9 780 998 420 241 GCAGGIGIATACATCCAAGCTCGTGAGGCTTTGCAAGGAGACACACGCCTTCAACTCCTA 300 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 938 120 180 818 9 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGAC 421 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGGGAAAATGAAATCCTGGATGAGTC Trefinaccesesceasceacecrescrisscrisscrisscrisasersaagacateceers GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTTGTGGGCACCAAAAGTGG 721 GICTGICATCGCATAIGICIACAAGAACCACICICIGGCCITIGIGGGCACCAAAGIGG CCTGCTCTTCACCGTCTTCTCCAAGGGCCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 121 CTICACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCACTT 181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA 639 GIICGCGIACGICTICCATGAGITCGIGGCCTCGATGATTAAGAICCCTTCGGACAC CTTCACCATCATCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCCACCAGGCTCCACCACGA CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAAGAACTCTGAGGCGGATGGCAT 781 CAAGCTGAAGAAG 793 661 1299 1359 819 (879 1059 481 1119 1179 1239 939 666 g g ઠે g ઠે 셤 ò 셤 $\dot{\delta}$ g ò g à ò ò g ò

RESULT 15 US-10-238-370-91 ; Sequence 91, Application US/10238370

CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058

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TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGC 360

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1179 CAGCAGIGCGCICTIAACCAIIGACGAIAACTICTGIGGCCIGGACAIGAAIGCICCCCI 1238 239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGACCGCATGAC 1298 1119 TIGITACCGGGGGAGGGACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 1359 CAAGCTGAAGAAG 1371 939 666 301 g qq à ద à ò Q 8 ò 8 8 셤 PUDDICATION NO. US20030073191A1

APPLICANT: Baker Kevin
APPLICANT: Baker Kevin
APPLICANT: Flivanoff, Ellen
APPLICANT: Flivanoff, Ellen
APPLICANT: Grimaddi, U. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Sang Zemin
APPLICANT: Christopher APPLICANT: Christopher
APPLICANT: Christopher Colin
APPLICANT: Christopher Colin
APPLICANT: Fong, Shemman
APPLICANT: Filling
APPLICANT: Christopher Colin
APPLICAN

Search completed: May 23, 2004, 13:05:11 Job time : 1470 secs 781 CAAGCTGAAGAAG 793

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GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGAACA

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579 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCCAAGAACTCTGAGGCGGATGGCAT 1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 639 GITCGCGTACGICTTCCATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 793; Conservative 0; Mismatches 0; Indels 0.

; TYPE: DNA ; ORGANISM: Homo Sapien US-10-238-370-91

241

879

TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGAA 240

TGTCTACTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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	Result No.	 	64	m	4	Ŋ	9	7	æ	on U	10	c 11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 98, Appl Sequence 98, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 42, Appl Sequence 42, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl Sequence 43, Appl Sequence 42, Appl Sequence 43, Appl Sequence 44, Appl Sequence 45, Appl	
US-09-639-206A-98 US-09-874-923-98 US-08-471-033-39 US-08-471-044-39 US-08-471-044-39 US-08-463-483A-39 US-08-463-483A-42 US-08-463-483A-39 US-08-471-046A-39 US-08-471-046A-39 US-08-471-046A-39 US-08-470-56B-39 US-08-470-56B-39 US-08-470-56B-42 US-08-470-56B-42 US-08-470-56B-42 US-08-470-56B-42 US-08-470-56B-42 US-08-470-56B-42 US-08-471-033-42 US-08-471-033-43	
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ALIGNMENTS

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Sequence 165, Application US/0990799A

Baten No. 665346

GREEAL INPORATION:
APPLICANT: Generated, Inc.
APPLICANT: Benovers, Luc
APPLICANT: Benovers, Luc
APPLICANT: Benovers, Luc
APPLICANT: Generated, Mary E.
APPLICANT: Grainald, Crimitopher J.
APPLICANT: Grainald, Vara J.
APPLICANT: Hilan, Kenneth, J.
APPLICANT: Hilan, Kenneth, J.
APPLICANT: Hilan, Kenneth, J.
APPLICANT: Hallan, Kenneth, J.
APPLICANT: Mather, Jenne P.
APPLICANT: Mood, William, I.
APPLICANT: Mood, William, P.
APPLICANT RELING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: US COVIGES
PRIOR PILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
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1996 GACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATAACTTCTGTGGACTGGACATC 2055
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
                                                                                                                       1636 rócecregadactrerreraciócreacecarcerécidederecidadadadades
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Pan, James
Pan, James
Pan, Nicholas F.
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Patent No. 6664376
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrara, Napoleone
Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan L
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Pred. No. 1.4e-131;
0; Mismatches 408;
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/VS99/23089
PRIOR PILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/VS99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/VS99/3091
PRIOR APPLICATION NUMBER: PCT/VS99/3099
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/VS99/3099
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PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: PCT/VS99/3099
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEX ID NOS: 423
LENGTH: 2477
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Best Local Similarity 67.1%;
Matches 837; Conservative
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; ORGANISM: Homo sapiens
US-09-907-794A-169
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Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Generatech, Inc.
APPLICANT: Botstein, David
APPLICANT: Benoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Eston, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                              GGGAAGCCCGAGTATTT
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Pred. No. 1.4e-131;
0; Mismatches 408;
                                           CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR PILING DATE: 2001-07-12
PRIOR PLING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-18
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-18
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR APPLICATION NUMBER: PCT/US99/28655
PRIOR APPLICATION NUMBER: PCT/US99/28055
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 199
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Best Local Similarity 67.1%;
Matches 837; Conservative
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: LENGTH: 2477

: TYPE: DNA

: ORGANISM: Homo sapiens

US-09-905-125A-169
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FILES REFERENCE: 1046-14
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Gao, Wei-Glang
Gerber, Hanspeter
Gerritsen, Mary E.
Godowski, Paul J.
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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CRGANISM: Homo sapiens
US-09-902-775A-169
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1832 GGGAATCTCCGACCCCGACACCTACACACATCTGGAAGACACAACAGCCTTCCTCTCCGGTT 1891
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EMB PC Compatible
OPERATING SYSTEM: PC-D0S/MS-D0S
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
FILING DATE: October 28, 1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Drovisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598)
APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598)
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GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Melanie F. DuBose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                               5241 TTGGGTCAACATGATCAAGAACCCGCAGTT
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; Sequence 1, Application US/09181706
; Patent No. 6130068
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
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STATE: WA
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: General General
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                      1348 ACCAAAAGTGGCAAGCTGAAGAACATCCGGGTGGATGGACCCAGGGGC 1395
                                                                                                                                                                                                                       2176 ACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC COMPATIBLE
COMPUTER: SYSTEM: PC COMPATIBLE
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION:
REPERENCE/CONTON NUMBER: ATTORNY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION NUMBER: PA-0001 US
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 603:
SUCHENCE CHARACTERICATION:
FROME COMPUTER: CALCATION FOR SEQ ID NO: 603:
SUCHENCE CHARACTERICATICS:
FROME COMPUTER: CALCATION FOR SEQ ID NO: 603:
SUCHENCE CHARACTERICATICS:
FROME COMPUTER: CALCATION FOR SEQ ID NO: 603:
SUCHENCE CHARACTERICATICS:
FROME COMPUTER: CALCATION FOR SEQ ID NO: 603:
SUCHENCE CHARACTERICATICS:
FROME COMPUTER: CALCATION FOR SEQ ID NO: 603:
SUCHARIA CALCATION FOR SEQ ID NO: 603:
                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-023-655-603
Sequence 603, Application US/09023655
Patent No. 6607879
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 64.4
Matches 440; Conservative
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CLONE: 3191066
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4817 ACGCAGTGAACAACTCCACCGTCTCCAGGACCTCAGCAAGTAATATGAAAACATGATCC 4876
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TTCAGCTTAATGAAATTGGTCTTGAGCTTCAAATGGGGACACGAGAAGAAGAACTTCTGG 3811
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Patent No. 6174689
GENERAL INPORMATION:
GENERAL SPELICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL EN
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                                                                                                                                                                                                                                                                                                                                                    Length 4707;
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3.5%; Score 201.2; DB 3;
Best Local Similarity 49.1%; Pred. No. 4.3e-39;
Matches 824; Conservative 0; Mismatches 728;
     NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFRENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
                                                          TELEPHONE: (206) 470-4189
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANBONESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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VIRAL ENCODED SEMAPHORIN PROTEIN
RECEPTOR DNA AND POLYPEPTIDES
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4637 CCAAAGCTGCAGATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGC 4696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3932 CAGATGTGGAGTACTC-----GGATGACCACTGCCATTTGATTTTA------ 3972
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                                                                    3452 AGACTGTCGGAGAGCCCTTCTATTTGCTGGTGACGACTCTGAACCAGAAATTAACAAGG 3511
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                                                                                                                                 4415 GCCCCATTGACGCCATCACGGGCGAGGCCCGCTACTCCTTGAGCGAGGACAAGCTCATCC
                                                                                                                                                                                    GTCCCGTGGATGTAATCACTTGCAAAGCCCTGTACACACTTAATGAAGACTGCTGTTGT
                                                                                                                                                                                                                                                        GCCAGCAGATTGACTACAAAACCCTGGTCCTGAGCTGTCAGCCCAGACAATGCCAACA
                                                                                                                                                                                                                                                                                                                         3572 GGCAGGTTCCGGAATTCAGTACTGTGGCATTAAACGTCGTCTTTGAAAAAATCCCGGAAA
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49.1%; Pred. No. 4.3e-39;
tive 0; Mismatches 728; Indels 126;
                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: MS.DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: «Unknown:
PRIOR APPLICATION NUMBER: 08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/ACTION: TAKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..4707
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                           ADDRESSEE: Janís C. Henry
STREET: 51 University St.
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206)470-4189
TELEFRX: (206)233-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRATURE:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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nes 824;
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| Sequence 1, Application US/09459066 |
| Patent No. 6187990 |
| GENERAL INFORMATION: |
| APPLICANT: Spriags, Melanie |
| TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN |
| TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES |
| NUMBER OF SEQUENCES: 10 |
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: STREET: 51 University St. |
| CITY: Seattle |
| STREET: WAR STREET: WAR STREET: WAS STREET: 
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Pred. No. 4.3e-39;
0; Mismatches 728;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEFOME: 206,470-4189
TELEFAX: (206)23-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
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Best Local Similarity 49.1%;
Matches 824; Conservative
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MOLECULE TYPE:
HYPOTHETICAL: N
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Patent No. 6562949

GENERAL INFORMATION

GENERAL INFORMATION

TITLE OF INVENTION: NETED ENCODED SEMAPHORIN PROTEIN

TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jamis C. Henry

STREET: Seattle

CITY: Seattle

STATE: WA

COUNTRY: US

ZIP: 98101

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS/Windows 95

CURRENTING SYSTEM: MS-DOS/Windows 95

CURRENTING SYSTEM: Windows 95

CURRENTING SYSTEM: Windows 95

CURRENTING SYSTEM: Windows 95

CURRENTING SYSTEM: US/09/459,065 FILING DATE:
CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION: NAME: Henry, Janis C REGISTRATION NUMBER: 34,347 REFERENCE/DOKET NUMBER: 2631 TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189 TELEPAX: (206)233-0644 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear RESULT 8 US-09-459-065-1 5297 4310 5357 4370 5417 5477 4136 5177 4250 4190 5237 QQ \triangle \trian d ŏ 셤 Q dd 6 B 6 $\dot{\delta}$ ò $\dot{\delta}$

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Pred. No. 4.3e-39;
0; Mismatches 728;
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                                                                                                                                                                                                               1..4707
MOLECULE TYPE: c
HYPOTHETICAL: NC
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US-09-459-065-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 824;
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TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1024)
CTHER INFORMATION: n = A,T,C or G

LENGTH:

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5356
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                                                 1877 GGTACACGGGCAGCCCCGACAGCCTCCGCTCACGGACACCTATGATCACTCCTGACCTGG 4936
                                                                                                                4937 AGAGTGGAGTCAAGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGGAGGAGG 4996
                                                                                                                                              ------ccagarrcegaagcarrccaagargrecaaggaaagagac-----arc 4015
                                                                                                                                                                                                              GAGGGAAGCACAAGTTCAAAGTAAAAGAAATGTATCTGACAAAGCTGCTGTCGACCAAGG 4075
                                                                                                                                                                                                                                                                                                                                                                                                              4370 AGCAGCAACTAGGGAAGGAAGCACCAACTAATAAGCTTCTCTATGCCAAGGATATCCCAA 4429
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3932 CAGATGTGGAGTACTC-----GGATGACCACTGCCATTTGATTTA-.
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APPLICANT: Astel, Jon. H.
APPLICANT: Astel, Jon. H.
APPLICANT: Carroll III, Eddie
APPLICANT: Endege, Wilson O.
APPLICANT: Endege, Wilson O.
APPLICANT: Ford, Donn E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
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TITLE OF INVENTION: GENES AND GENES A
RESULT 9
US-09-328-475C-37/C
19-328-475C-37/C
5 Sequence 37, Application US/09328475C
7 Patent No. 6476207
7 GENERAL INFORMATION:
APPLICANT: Zhang, Jimmy
APPLICANT: Astel, Jon H
7 APPLICANT: Carroll III, Eddie
7 APPLICANT: Carroll III, Eddie
7 APPLICANT: Endee, Wilson O.
8 APPLICANT: Carroll III, Eddie
8 APPLICANT: Astel
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US-08-232-463-14/c ; Sequence 14, Application US/08232463 ; Patent No. 5670367

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4744
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Sequence 6281, Application US/09313294A

Sequence 6281, Application US/09313294A

Sequence 6281, Application US/09313294A

SEQUENCE SAFETICANT: Lady Sequence PL-0017 US

TITLE OF INVENTYON: DOLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR TILE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL Program

SEQ ID NO 6281

LENGTH: 288
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OTHER INFORMATION: Incyte ID No. 6476212 700351536H1

NAME/KEX: unsure

NAME/KEX: unsure

LOCATION: 9, 19, 26, 50, 82, 109, 135, 175-176, 186, 197, 208, 217, 244

OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-6281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 GGGTCGINCTGCAANATGAGGACATCACCAACAATINAGGGTGACTGGAAGCGGCTCA
                                                                                                                                                                                   TICAACACCATGAGTGCACTCTCAGAGATCTTCTCCTATGTGGGCAAATACAGCGAGGAG
                                                                                                                                                                                                             720 TTCAACATGTTGAGTGCCCCCAATGAGATCTACTCCTATGTCAGCAAGTATAGTGAGGAG
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                                                                                         5472 CAGCGACCAAGACATGAACGCATA-CCTGGCTGAGCAGTCCCGGATGCACATGAG-
                                                                                                                                  780 cagreaccadeccareaareccracerreeceaecaereceeerecaeneeres
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    Length 1024;
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1.0%; Score 57.8; DB 4;
Best Local Similarity 73.2%; Pred. No. 0.00013;
Matches 71; Conservative 0; Mismatches 26;
Score 86.4; DB 4;
Pred. No. 2.4e-11;
0; Mismatches 68;
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  Query Match 1.5%;
Best Local Similarity 67.9%;
Matches 148; Conservative
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Sequence 3, Application US/08607509
Sequence 3, Application US/08607509
Patent NO. S8767104.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4049 AAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAACAAGGTGTTCCTGCTGTTCTTCATCC
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Pred. No. 0.034;
0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
CONFRANTO SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,509
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTON REVARATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.404C3
TELECOMMUTCATION INFORMATION:
                                       5009 GCAAGATGGTGTCTGAATCTACCTGACCCGACTCCTG 5046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1867 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%;
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Matches 179; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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FEATURE:
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US-08-607-509-3
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                                                                                                                                                      RESULT 12
US-08-607-509-3
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                                                          임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4949 AGATGTGGCACCTAGTGAAGAACCACGAGCACGGAGACCAGAAGGAGGGGGGACCGGGGGA 5008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1709 TCACCACCAAGATTGAAAATGATTGGAAGCGACTGAACACACAGTGGCCCACTACCAGGTGC 4768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4829 ACTCCACCGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGCA 4888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4769 CAGATGGTTCCGTGGTGGCATTAGTGTCCAAGCAGGTGACAGCCTATAACGCAGTGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4649 ATATGGATCTGGAGTGGCGACAAGGAAGTGGGGCAAGGATGATCTTGCAGGATGAAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.9%; Score 49.6; DB 1; Length 7 Best Local Similarity 4.0%; Pred. No. 0.058; Matches 16; Conservative 219; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                 ZUE: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
   GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: CREBIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFELIAND DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE:
FILING DATE:
FILING BATE: 26-AUG-1991
ATTORNEY, AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTAATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9900
TELEFAX: (703)836-9109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: ...
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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RESULT 17

US-08-989-370-3

; Sequence 3, Application US/08989370
; Patent No. 6012468
; Patent No. 6012468
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
; TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
; TITLE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
; ADDRESSEE: SEED and BERRY
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4289 CTGAGTCAGTGGCTGAGAAGATGCTGACCAATTGGTTTACTTTCCTCCTCTACAAGTTCC 4348
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         4349 TCAAGGAGTGTGCTGGGAGGCCCCTCTTCTCCCTGTTGTGCCATCAAGCAGCAGAAGG 4408
                                                             703 rccerrccreccanadahcarccagrccacrtcrrcrcccccacaadahdahda 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4049 AAGGCCTGAAGCTCTTCGCCCAGCTCATCAACAAGAGGTGTTCCTGCTGTCCTTCATCC
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Pred. No. 0.034;
0; Mismatches 216; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle
STATE: Washington
COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CLASSIEICATION:
CLASSIEICATION:
CLASSIEICATION:
CLASSIEICATION:
                                                                                                                                       1409 AGAAGGGCCCCATTGACGCCATCACGGGCGAGGCC 4443
                                                                                                                                                                                             763 TACTGGAGCTGACGAAGAAGTTCATGCGCGACCCC 797
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NAME: Maki, David J.
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
RELECAMINICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-631
INFORMATION FOR ESQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 45.3%;
Matches 179; Conservative
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US-08-989-370-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642
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103 TCCGCTTCCTGCCGAAGGACATCCAGGTCGCGCTCTTCTCCGCCACGATGCCGGAGGAGG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 GCATCGGTGAGTTCCTGTCGAACAGCTCCAAGTTCTGCGAGACCTTTGTCGGCGCGCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1169 TCATGACCGTGCTGCAAGCTGGAGTACGCCACTGATGTGCTGAAGCAGCTGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ses eccecererceacerearcaacerescerescerecerescacacacacacacacacaceres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49.4; DB 2; Length 1867; Pred. No. 0.034; 0; Mismatches 216; Indels 0
                                                                                                                                                                Sequence 3, Application US/08634642

Sequence 3, Application US/08634642

Patent No. 5879687

GENERAL INFORMATION:
FREED STATE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
SEED and BERRY LLP
STREET: Seattle
CITY: Seattle
STREET: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/634,642

FILING DATE: 18-APR-1996

CLASSIFICATION: 424

ATTORNEY/AGBMT INFORMATION:

NAME: Mark, David J.

REFERENCE/POCKET NUMBER: 31,392

REFERENCE/POCKET NUMBER: 31,392

REFERENCE/POCKET NUMBER: 31,392

REFERENCE/POCKET NUMBER: 31,392

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 682-6031

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTER.STICS:

LENGTH: 1867 bese pairs

TYPE: mucleic acid

TYPE: MUCLE CACID

                                                                1409 AGAAGGCCCCCATTGACGCCATCACGGCGAGGCC 4443
                                                                                                                          763 TACTGGAGCTGACGAAGAAGTTCATGCGCGACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.3%;
Matches 179; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , LOCATION:
US-08-634-642-3
                                                                                                                                                                                                                    RESULT 13
US-08-634-642-3
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Search completed: May 23, 2004, 11:09:07
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US-09-388-169-3
Sequence 3, Application US/09398169
Sequence 3, Application US/09398169
Sequence 4, Application US/09398169
Sequence 5, Application US/09398169
STATE OF INVENTION: METHODS FOR ENHANCEMENT OF PROTECTIVE IMMUNE RESPONSES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatle
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DATE: TYPE: Floppy disk
COMPUTER: DATE: TYPE: PLOPPY disk
COMPUTER: DATE: TYPE: TO-DOS/MS-DOS
SOFTWARE: PATEINIR Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/398,169
FILING DATE: 17-Sep-1999
SPILOR APPLICATION NUMBER: US/09/398,370
FILING DATE: 12-DEC-1997
ATTOMET/AGENT INFORMATION:
NUMBER MATEUR TABLE TO-DEC-1997
ATTOMET/AGENT AND THE TO-DEC-1997
ATTOMET/AGENT TO-DEC-1997
ATTOMET/AGENT TO-DEC-1997
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643 IGCTCGACGAGGCTGATGAGATGCTGTCTCGGGGCTTCGCGGACCAGATTACGAGATCT 702
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Best Local Similarity 45.3%; Pred. No. 0.034;
Matches 179; Conservative 0; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MAKI, DAVIG J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.404C5
RELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6910
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER/STICS:
LENGTH: 1867 base pairs
TYPE: nucleic acid
STRANDENSS: single
                                                                                                                                                                                                                                                                         4409 AGAAGGGCCCCATTGACGCCATCACGGCCGAGGCC 4443
                                                                                                                                                                                                                                                                                                                                                  763 TACTGGAGCTGACGAAGAAGTTCATGCGCGACCCC 797
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INAME/KEY: CDS

LOCATION: 117..1325

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-398-169-3
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1229 CCGACCTCATTGACAAGAACCTGGAGAGAAAGAACCACCCTAAAGCTGCTGCTCAGGAGGA 4288
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May 23, 2004, 10:03:08 ; Search time 1467 Seconds (without alignments) 17630.569 Million cell updates/sec
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5691
1 atgaaagccatgccctggaa......gcttagacagctgaaataaa 5691
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    2953838 segs, 2272363821 residues
                                                                            using sw model
                                                                                                                                                                                                                                                                           IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                            - nucleic search,
                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                           Scoring table:
                                                                            OM nucleic
                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Published Applications NA:*

| cgn2_6/ptodata/2/pubpna/USO7_PUBCONB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/USOB_NEW_PUB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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Result No.	Score	% Query Match	% Query Match Length DB	DB	ΩI	Description		,
¦	5691	100.0	i	133	US-09-964-956-12	Sequence 1	12,	Appl
N	5680.6	99.8	6367	17	US-10-451-010-19	Sequence 1	19,	Appl
m	2778.4	48.8	6730	15	US-10-175-523-95	Sequence	95,	Appl
4	2659.4	46.7	6147	13	US-10-312-352-70	Sequence	70,	Appl
Ŋ	2533.8	44.5	5895	13	US-10-087-684-31	Sequence	31,	Appl
ų	2533.8	44.5	5895	13	US-10-218-779-31	Seguence	31,	Appl
r	1157.8	20.3		16	US-10-108-260A-802	Sequence	802,	
œ	793.8		2597	13	US-10-245-752-91	Sequence	91,	Appl
σ	793.8			13	US-10-245-859-91	Sequence	91,	Appl
10	793.8			15	US-10-245-103-91	Sequence	91,	Appl
11	793.8	13.9	2597	15	US-10-245-107-91	Sequence	91,	Appl
12	793.8			15	US-10-245-143-91	Seguence	91,	Appl
13	793.8			15	US-10-245-771-91	Sequence	91,	Appl
14	793.8			15	US-10-245-851-91	Sequence	91,	Appl

91,	Sequence 91, Appl	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	91,	equence 91,	91,
US-10-245-883-9	5 US-10-237-535-91	US-10-238-183-9	US-10-238-283-9	US-10-238-370-9	US-10-245-055-9	US-10-245-147-9	US-10-245-730-9	US-10-245-739-9	US-10-246-210-	US-10-239-196-	US-10-243-024-	US-10-243-409-	US-10-245-621-	US-10-245-880-	US-10-245-033-9	US-10-243-095-	US-10-245-185-9	US-10-245-427-	US-10-245-473-	US-10-245-770-9	US-10-245-877-9	US-10-246-976-9	US-10-243-320-	US-10-242-743-9	US-10-242-845-9	US-10-237-636-9	US-10-238-325	US-10-238-346-9	US-10-238-411	US-10-243-12
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ALIGNMENTS

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APPLICANT: Matcheaula APPLICANT: Matcheaula APPLICANT: Matcheaula APPLICANT: Matcheaula APPLICANT: Milet, Isabelle APPLICANT: Milet, Isabelle APPLICANT: Milet, Isabelle APPLICANT: Milet, Isabelle APPLICANT: Stone, David APPLICANT: Grosse, Miliam M APPLICANT: Grosse, Miliam M APPLICANT: Eleptew, Denise M APPLICANT: Eleptew, Denise M APPLICANT: Rekude M Randerly M APPLICANT: Rekude M Ratin D Badgaru, Muralidhara APPLICANT: Rekude M Ratin D APPLICANT: Spycek, Kimberly A APPLICANT: Shinkerts, Richard A APPLICANT: Shinkerts, Richard A APPLICANT: Shinkerts, Richard A APPLICANT: Shinkerts, Rolland A A APPLICANT: Shinkerts, Rolland A A APPLICANT: Shinkerts, Rolland A APPLICANT: Solot-09-27 PRIOR FILING DATE: 2000-09-27 PRIOR FILING DATE: 2000-09-27 PRIOR FILING DATE: 2000-09-27 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: 60/236,065 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: 60/236,066 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: 60/236,066 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICANTION NUMBER: 60/236,066 PRIOR FILING DATE: 2000-09-27 PRIOR PRIO
RESULT 1
US-09-964-956-12
'Sequence 12, Application US/09964956
'Publication No. US20040043926A1
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
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Page 2

661 GAGTTGGTGGCCTGGATGATTAAGATCCCTTCGGACACCTTCACCATCATCCTGACTTT 720 721 GATATCTACTATGTCTATGGATTTAGCAGTGCCAACCTTGTCTACTTTTTGACCCTCCAA 780 721 GATATCTACTATGTCTATGGATTTTAGCAGTGCCAACTTTGTCTACTTTTTGACCCTCCAA 780 721 GATATCTACTATGTCTATGGATTTTAGCAGTGCCAACTTTGTCTACTTTTTGACCTCCAA 780 781 CCTGAGATGGTGTCTCCACCACACCACCAAGTGTATACATCCAAGTT 80	781 CCTGAGATGGTGTCCCACCAGGCTCCACCAGGAGGAGGTATACATCCAAGGTC 840 841 GTGAGGCTTTGCAAGGAGGACACAGCTTCAACTCCTATGTAGAGGTGCCCATTGGCTGT 900 841 GTGAGGCTTTGCAAGGAGACACAGCTTCAACTCCTATGTAGAGGTGCCCATTGGCTGT 900 841 GTGAGGCTTTGCAAGGAGACACAGCTTCAACTCCTATGTAGAGGTGCCCATTGGCTGT 900	GAGCGCAGTGGGGTGGAGTACCGCCTGCTGCTGCCTACCTGTCCAAAGCGGGGGCC 960	961 GIGCTIGGCAGGACCCTIGGAGICCATCCAGAIGATGACCTGCTCTTCACCGICTTCTCC 1020	1021 AAGGGCCAGAAGGGGAAATGAAATCCTGGATGAGTCGGCCCTGTGCATCTTCATCTTG 1080 1021 AAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTCGGCCCTGTGCATCTTCATCTTG 1080	AAGCAGATAAATGACGGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGCACG H		GACGATAACTICTGTGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGT [GGAATTCCCGTCTTCACGGAGGACGGCGCGTGACGTCTCTCATCGCGTATGTCTACGGATATGTCTACGGATGTCTTACGGAGGACGGGATGACGTTGTCTTCTCTCTC	AAGAACCACTCTCTGGCCTTTGTGGCCACCAAAGTGGCAAGCTGAAGAAGATCGGGTG [GATGGACCCAGGGGCACCTCCAGTATGAGACGGTGGTGGTGGTGGTGGTCCGGGCCCCGGGGTGGTGGTG	GTCCTCCGGGATATGGCCTTCTCCAAGGACCACGAGGAACTCTACATCATGTCAGGAGG [cagcicaccagastcccigigaagiccigigagichii	Gectchegegreececartgroectectgractgrachgrachachachagad	CGGTGTCAGCGGTCCAAGGAGCCCCGCAGGTTTGCCTCGGAGGTGAAGCAGGTGTGTGT	CTGACGGTCCATCCCAACAATATCTCCGTCTCTCAGTACAACATCTGTGTTTTTTTT	1741 ACGTACATGTCCCGGAGGTGTCACCTCGACCTTTGAGGACCTGTAGAGA 1800
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PRIOR APPLICATION NUMBER: 60/236,135 PRIOR FILING DATE: 2000-09-28 PRIOR APPLICATION WUMBER: 60/237,434 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/238,321 PRIOR ELING DATE: 2000-10-05 PRIOR PLICATION NUMBER: 60/238,399 PRIOR FILING DATE: 2000-10-06	PRIOR APPLICATION NUMBER: 60/238,396 PRIOR FILING DATE: 2000-10-06 PRIOR PLILING DATE: 2001-3-16 PRIOR FILING DATE: 2001-03-16 PRIOR APPLICATION NUMBER: 60/294,823 PRIOR FILING DATE: 2001-05-31	PRIOR APPLICATION NUMBER: 60/304,868 PRIOR FILING DATE: 2001-07-12 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 12	LENGTH: 5691 TYPE: DNA ORGANISM: 1-mmo sapiens	ery Matc st Local	AACTGGACCTGCCTTCTCCCACCTCCTCATGGTGGGCATG 60 AACTGGACCTGCCTTCTCTCCCACCTCCTCATGGTGGGCATG 60	61 GGCTCCTCCACCTTTGCTCACCCGGCAGCCCCGCTGTCCCAGAAGCAGCGCGGTCATTT 120 		GGACACATTTACTTGGGGGCCGTCAATCGGATTTACAAGCTCTCCCGCGACCTGAAGGTC	241 TTGGTGACGCATGAGACCAGGACGAGGACAACCCCAAGTGTTACCCACCC	301 GTCCAGACCTGCAATGAGCCCCTGACCACCACAACAATGTCAACAGATGCTCCTCATA 360 		CTGAGGCTGGAGGACCTCTTCAAGCTGGGGGAGCCTTATCATAAGAAGGAGCAC 	Oy 481 TCAGGTGTCAAGAGGGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540 Db 481 TCAGGTGTCAAGAGGGGCTCAGTCTTTGGAGTGATCGTCTCCTACAGCAACCTGGAT 540	541 GACAAGCTGTTCATTGCCACGGCAGTGGATGGGAAGCCCGAGTATTTTCCCACCATCTCC 600	601 AGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATGTTCGCGTACGTCTTCCATGAT 660 	661 GAGTICGIGGCCICGATGATTAAGAICCCTICGGACACCTICACCAICAICCCIGACTII 720

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                                                                         CIGACGGICCAICCCAACAATAICTCCGICICTCAGIACAACGIGCIGCIGGICCIGGAG
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1526 GIGCITGGCAGGACCCTTGGAGTCCATCAGATGATGATGATGACGCTCTTCACCGTCTTTCTCC
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FILE REFERENCE: PF-0867 USN
CURRENT APPLICATION NUMBER: US/10/451,010
CURRENT FILING DATE: 2003-06-17,
PRIOR PAPLICATION NUMBER: PCT/US01/49206
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL PROGRAM
SEQ ID NO 19
INMUMER OF SEQ ID NOS: 20
SOFTWARE: PERL PROGRAM
SEQ ID NO 19
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COFTWARE: PERL PROGRAM
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COFTWARE: MASC feature
OWARLKEY: misc feature
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OWHER INFORMATION: Incyte ID NO: 7156379CBI
PERTURE:
NAME/KEY: unsure
INFORMATION: 166
INFORMATION: A, t, c, g, or other
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         NUMBER OF SEQ ID NOS: 197

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SEQ ID NO 95

LENGTH: 6730

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(6730)

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US-10-175-523-95
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin version 3.1
SEQ ID NO 95
LENGTH: 6730
                                                                                   Query Match
Best Local Similarity 69.3%;
Matches 3858; Conservative
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Gregory A.
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; TYPE: DNA; ORGANISM: Homo sapiens; FEATURE: FEATURE: NAME/KEY: misc_feature; OTHER. INFORMATION: Incyte ID No. US20040053824A1 7204554CB1 US-10-312-352-70
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                                     Score 2659.4; DB 13
Pred. No. 0;
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Best Local Similarity 68.4%;
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CAATTGGTTTACTTTCCTCTCTACAAGTTCCTCAAGGAGTGTGCTGGGGAGCCCCTCTT

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----GGGGCCTGCCTCAGGCCTCAGGGCCCAGGGCCCAGGAGCGCCCAGGAGCCCCAGGAGCCCCAGGAGCCCCAGGAGCCCCAGGAGCCCCAGGAGCCCCAGGAGCCCCAGGAGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCA CCGGGATATGGCCTTCTCCAAGGACCACGAGCAACTCTACATCATGTCAGAGAGGCAGCT defigercaacaadadacigaacifedareareeeeeeaaaredardaaaariteid

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APPLICANT: Zerhusen, Bryan
APPLICANT: Malyankar, Uriel
APPLICANT: Genuse, Bryan
APPLICANT: Gonovia
APPLICANT: Gonovia
APPLICANT: Miller, Charles
APPLICANT: Miller, Baha
FILLE REPERENCE: 21402-114
CURRENT FILLNG DATE: 2002-08-14
CURRENT FILING DATE: 2000-11-29
PRIOR PELING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/254,180
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR PELING DATE: 2001-01-25
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GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit
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Padigaru, Muralidhara
Mishra, Vishnu
Patturajan, Meera
Shenoy, Suresh
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Grosse, William
Alsobrook II, John
Lepley, Denise
Rieger, Daniel
Burgess, Catherine
Casman, Stacie
Spytek, Kimberly
Boldog, Ferenc
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Rastelli, Luca
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Millet, Isabelle
Ellerman, Karen
Stone, David
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APPLICANT: BAKEL'KEVIN
APPLICANT: BAKOL'NE'
APPLICANT: Filvaroff, Ellen
APPLICANT: Galdard, Audrey
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Shith, Victoria
APPLICANT: Stephan Jean-Phillippe
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APPLICANT: Abang, Zemin
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 1002-09-16
CURRENT FILING DATE: 2002-09-16
PRIOR PILLNG DATE: 2002-09-16
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Matches 795; Conservative 0; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PILING DATE: 1997-11-10
PRIOR PILING DATE: 1997-11-10
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PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-08
PRIOR APPLICATION NUMBER: 60/089801
PRIOR PILING DATE: 1998-06-18
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RESULT 10
US-10-245-103-91
i Sequence 91, Application US/10245103
i Publication No. US20030068778A1
i GENERAL INFORMATION:
APPLICANT: Bater, Keavin
APPLICANT: Flavaroff, Ellen
APPLICANT: Grimald, J. Christopher
APPLICANT: Grimald, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Scephan, Jean-Phillippe
APPLICANT: Anabe, Colin
APPLICANT: Mood, William
APPLICANT: Mood, William
APPLICANT: Mood, William
APPLICANT: Mood, William
APPLICANT: ACABOR SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION UNBER: US/10/245,103
CURRENT APPLICATION NUMBER: US/10/245,103
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/059114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1059 GGCCCTGTGCATCTTGATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGGTGCAGTC 1118
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121 GTCTGTCATCGCATATGTCTACAAGAACCACTCTGGCCTTTGTGGGCACCAAAAGTGG 780
                                                                                                                                                                                                                            819 GCAGGIGIATACATCCAAGCTCGIGAGGCTTTGCAAGGAGGACAGCAGCCTTCAACTCCTA 878
241 GCAGGIGIATACATCCAAGCTCGIGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300
                                                                                                                                                      879 IGINGAGGIGCCCATIGGCTGIGAGCGCAGIGGGGIGGAGIACCCCCCTGCIGCAGGCTGC 938
                                                                                                                                                                       301 IGHAGAGGGCCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCTGCAGGCTGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                      601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 GGGAGTGTCCGACATGGTGGGTGGAATTCCCGTCTTCACGGAGGAGGACGGGACCGCATGAC
CTTCACCATCATCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT
                                                                                                                                                                                                                                                                     CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC
                                                                                                                                                                                                                                                                                  421 CCTGCTCTTCACCGTCTTCTCCAAGGCCAGAAAAGGGAAAAATGAAAATCCCTGGATGAGTC
                                                                                                                                                                                                                                                                                                                                              481 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC
                                                                    181 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGA
                                                                                                                                                                                                             1119 TIGITACCGGGGCGAGGCCACGCTGGACCTGGCTCAAGGTGAAGGACATCCCCTG
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                                                                                                                                                                                                                           Eaton, Dan
Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
                                                                                                                                                                    Sequence 91, Application US/10245859
Publication No. US20030064474A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
                                                                      1359 CAAGCTGAAGAAGATCC 1375
                                                                                               781 CAAGCTGAAGAAGGTGC 797
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Best Local Similarity 99.7°
Matches 795; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2597
TYPE: DNA
CRGANISM: Homo Sapien
US-10-245-859-91
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APPLICANT: EltoxOff, Ellen
APPLICANT: Godard, Audrey
APPLICANT: Gordard, Audrey
APPLICANT: Grimel, Audrey
APPLICANT: Grimel, Audrey
APPLICANT: Grimely, Austin
APPLICANT: Gran-Phillippe
APPLICANT: Stephan, Gean-Phillippe
APPLICANT: Stephan, Gean-Phillippe
APPLICANT: Macable, Colin
APPLICANT: Macable, Aultian
APPLICANT: Macable, Aultian
APPLICANT: Fond Shewman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
CURRENT APPLICATION WHOER: US/10/245,107
CURRENT FILING DATE: 12002-07-18
FRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 12097-09-17
PRIOR PLING DATE: 12097-09-17
PRIOR PLING DATE: 12997-10-24
PRIOR PLING DATE: 12997-10-24
PRIOR PLING DATE: 1298-06-25
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PLING DATE: 1298-06-24
PRIOR PLING DATE: 1298-06-25
PRIOR PLING DATE: 1298-06-26
PRIOR PLING DATE: 1208-06-26
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PLING DATE: 1208-06-26
PRIOR 
                         GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGACCGCATGAC 1298
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                                                                                      GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGACAGCGCATGAC
                                                                                                                                                                                                            GICTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 91, Application US/10245107
Publication No. US20030068779A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              CAAGCTGAAGAAGATCC 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781 CAAGCTGAAGAAGGTGC 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-10-245-107-91
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR PILING DATE: 1997-10-0-4
PRIOR PELICATION NUMBER: 60/055027
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR PLING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-02
PRIOR PLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-18
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
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US-10-245-103-91
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PRIOR APPLICATION NUMBER: 10/197942

PRIOR FILING DATE: 2002-07-18

PRIOR PELING DATE: 2002-07-18

PRIOR PELING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR PELICATION NUMBER: 60/065027

PRIOR PELING DATE: 1997-11-10

PRIOR PELING DATE: 1998-06-02

PRIOR PELING DATE: 1998-06-04

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-18

PRIOR PELING DATE: 1998-06-24

PRIOR PELING DATE: 1998-06-25

PRIOR PELING DATE: 1998-06-25
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US-10-245-143-91
US-10-245-143-91
Sequence 91, Application US/10245143
Publication No. US20030068780A1
SENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Goddard, Auderin
APPLICANT: Goddard, Auderin
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Sheman
APPLICANT: Sheman
APPLICANT: Anang, Zemin
APPLICANT: ANANGMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
FILE REFERENCE: PS 33031020
CURRENT FILING DATE: 2002-09-16
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               GITCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC
                                                                                                                                                          TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCCACCAGGCTCCACCACGAGGA
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                                                                                              CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT
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RESULT 13
US-10-245-771-91
'Sequence 91, Application US/10245771
'Publication No. US20030068781A1
'GENERAL INFORMATION:

APPLICANY: Baker, Kevin
APPLICANY: Baker, Kevin
APPLICANY: Baker, Kevin
APPLICANY: Baker, Kevin
APPLICANY: Goddard, Addrey
APPLICANY: Goddard, Addrey
APPLICANY: Goddard, Addrey
APPLICANY: Goddard, Addrey
APPLICANY: Smith Victoria
APPLICANY: Smith Victoria
APPLICANY: Stepha, Gean Phillippe
APPLICANY: Watanbe, Colin
APPLICANY: Watanbe, Colin
APPLICANY: Range Sherman
APPLICANY: NUNER: USD SCRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: USJ 10/197942
FRICK APPLICATION NUMBER: 10/197942
FRICK APPLICATION NUMBER: 10/197942
FRICK FILING DATE: 1099-00-16
FRICK APPLICATION NUMBER: 60/063046
FRICK APPLICATION NUMBER: 60/06304
FRICK APPLICATION NUMBER: 60/06304
FRICK APPLICATION NUMBER: 60/06304
FRICK APPLICATION NUMBER: 60/06304
FRICK APPLICATION NUMBER: 60/08901
FRICK FILING DATE: 1998-05-22
FRICK FILING DATE: 1998-05-25
FRICK APPLICATION NUMBER: 60/09069
FRICK FILING DATE: 1998-06-25
FRICK FILING DATE: 1998-06-25
FRICK FILING DATE: 199

TYPE: DNA
CORGANISM: Homo Sapien
US-10-245-771-91

Gaps ô 13.9%; Score 793.8; DB 15; Length 99.7%; Pred. No. 6.3e-220; tive 0; Mismatches 2; Indels Query Match Best Local Similarity 99.7 Matches 795; Conservative

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DB 15; Length 2597;

1119 TTGTTACCGGGGGGGGGGCGCCTGGACCTGGCTCAAGGTGAAGACACTCCCTG 1178 GTCTGTCATCGCATATGTCTACAAGAACCACTCTGGCCTTTGTGGGCACCAAAAGTGG 1358 1058 1059 GGCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGCT 1118 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT 1238 1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGACCGCATGAC 1298 601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCT 660
 879
 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGTGCAGTACCGCCTGCTGCAGGCTGC
 938

 301
 TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGAGTGCAGTACGCCTGCTGCTGCAGCTGC
 360
 421 CCTGCTCTTCACCGTCTTCTCCAAGGCCCAGAAGGCGGAAAATGAAATCCCTGGATGAGTC 480 661 GGGAGTGTCCGACATGGTGGTGCTGGAATTCCCGTCTTCACGGAGGACAGGACGCCCATGAC 720 721 GTCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGG 780 759 TGTCTACTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGGTCCCACCACCACGAGGA 818
181 TGTCTACTTTTTGACCCTCCAACCTGAGATGTGTGTCTCCACCAGGCTCCACCACCACGAGGA 240 241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTA 300 180 61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC CITCACCATCATCCCTGACTITGATATCTACTATGTCTATGGTTTTAGCAGTGCCAACTT CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT CAAGCTGAAGAAGATCC 1375 1179 1299 1359 121 819 669 à 8 8 8 8 gg 셤 ò g 임 ठ व ठ සු දු g ઠે qq ઠે a ò ઠે ઠે d 8 8

US-10-245-851-91
Sequence 91, Application US/10245851
Sequence 91, Application US/10245851
Sequence 91, Application US/1020806878241
Sequence 91, Application No. US2003006878241
Sequence 91, Application No. US2003006878241
APPLICANT: Baker, Kevin
APPLICANT: Filvaroff, Ellen
APPLICANT: Grinmaldi, J. Christopher
APPLICANT: Smith, Vactoria
APPLICANT: Smith, Vactoria
APPLICANT: Smath, Vactoria
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Scong, Sherman
APPLICANT: ALSONG, Sherman
APPLICANT: ALSONG SHERMEN AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME

GREATEAL INCRAFATION:

APPLICANT: Baker, Kevin

APPLICANT: Baker, Kevin

APPLICANT: Baton Dan

APPLICANT: Filvaroff Bllen

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Smith, Yactoria

APPLICANT: Smith, Yactoria

APPLICANT: Shang, Zemin

APPLICANT: Zhang, Zemin

APPLICANT: APBC, SERETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

THIE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

THIE OF INVENTION: SECRETED AND TRANSMEMBRANE

PILK BPLICANT: DAGE: 2002-09-16

PRIOR APPLICANTON NUMBER: 10/197942

PRIOR APPLICANTON NUMBER: 60/065914

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-11-10

PRIOR PLING DATE: 1998-06-22

PRIOR PLING DATE: 1998-06-18

PRIOR PLING DATE: 1998-06-25

PRIOR PLING DATE: 1998-06-25 1239 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGACCGCATGAC 661 GGGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACGAGGACGGCATGAC TTGTTACCGGGGCGAGGCACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTG 601 CAGCAGTGCGCTCTTAACCATTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCT Length 2597; , 0 Indels Query Match
13.9%; Score 793.8; DB 15;
Best Local Similarity 99.7%; Pred. No. 6.3e-220;
Matches 795; Conservative 0; Mismatches 2; I 1179 CAGCAGTGCGCTCTTAACCATTGACGATAACT US-10-245-883-91 ; Sequence 91, Application US/10245883 ; Publication No. US20030068783A1 ; GENERAL INFORMATION: 1359 CAAGCTGAAGAAGATCC 1375 781 CAAGCTGAAGAAGGTGC 797 TYPE: DNA
CORGANISM: Homo Sapien
US-10-245-883-91 541 g g 유 ઠે 8 Š ò 999 CCTGCTCTTCACCGTCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTC 1058 TTGTTACCGGGGCGAGGGCACGCTGGACCTGGCTCAAGGTGAAGGACATCCCCTG 1178 1059 GGCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTC 1118 818 240 878 938 639 GITCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 698 61 GTTCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACAC 120 758 121 CTTCACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 180 300 9 FILE REFERENCE: P3630RLC93
CURRENT APPLICATION WOMBER: US/10/245,851
CURRENT FILING DATE: 2002-09-16
FRIOR APPLICATION NUMBER: US/10/19742
FRIOR APPLICATION NUMBER: 06/059114
FRIOR FILING DATE: 1997-09-17
FRIOR PELING DATE: 1997-09-17
FRIOR PELING DATE: 1997-10-14
FRIOR APPLICATION NUMBER: 66/065027
FRIOR APPLICATION NUMBER: 66/065027
FRIOR APPLICATION NUMBER: 66/065027
FRIOR APPLICATION NUMBER: 66/079689
FRIOR APPLICATION NUMBER: 66/079689
FRIOR FILING DATE: 1998-03-27
FRIOR FILING DATE: 1998-06-02
FRIOR PELING DATE: 1998-06-18
FRIOR PELING DATE: 1998-06-18
FRIOR PELING DATE: 1998-06-18
FRIOR FILING DATE: 1998-06-24
FRIOR FILING DATE: 1998-06-24
FRIOR FILING DATE: 1998-06-25
FRIOR FILING DATE: 1908-06-25
FRIOR FILING DATE: 1908-06-25 759 IGICTACTITITGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACGAGGA
181 IGICTACTITITGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACGAGGA. GGCCCTGTGCATCTTCATCTTGAAGCAGAAAAAAGCGCGCATTAAGGAGCGGCTGCAGTC 241 GCAGGTGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACACAGCCTTCAACTCCTA 579 CGAGTATTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT 1 CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCAT CTICACCAICATCACCCTGACTITGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTT 819 GCAGGIGTATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACACCCTTCAACTCCTA TGTAGAGGTGCCCATTGGCTGTGAGCGCAGTGGGGGTGGAGTACCGCCTGCTGCAGGCTGC CCTGCTCTTCACCGTCTTCTCCCAAGGCCAGAAGCGGAAATGAAATCCCTGGATGAGTC 0; Gaps Query Match
13.9%; Score 793.8; DB 15; Length 2597;
Best Local Similarity 99.7%; Pred. No. 6.3e-220;
Matches 795; Conservative 0; Mismatches 2; Indels 0; ; SEQ ID NO 91 | LENGTH: 2597 | TYPE: DNA | ORGANISM: Homo Sapien | US-10-245-851-91 879 686 421 481 1119 669 g ò 9 ŏ g 8 6 8 6 8 6 8 6 ò q à

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Gaps

Search completed: May 23, 2004, 11:33:54 Job time : 1479 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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Run on: May 25, 2004, 03:45:17; Search time 29 Seconds (without alignments)
3375.270 Million cell updates/sec
Title: US-09-964-956-13
Sequence: MKAMPWNWTCLLSHLLMVGM.....QKLAYKLEQVITLMSLDSNK 1896
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100*

Maximum Match 100*

Listing first 45 summaries

Database : Issued Patents AA:*

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/RCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Segnence	Seguence	Sequence	Sequence	Sequence	Sequence
ΙD	US-09-907-794A-170	39-905	-09-902-775A-17	-09	US-09-458-791-2	-455	09-455	-345-473	38-556	US-09-077-940A-4	US-09-077-940A-2	US-09-653-274-4	US-08-121-713D-62	US-08-835-268-62	φ	-391-6	060-610-	PCT-US94-10151A-62	-09-623	US-09-653-274-8	-08-123	-08-835-268-5	-692	-08-833-391-5	US-09-060-610-58	PCT-US94-10151A-58	US-08-121-713D-54
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Score	1351.5	1351.5	1351.5	1349	1349	1349	1349	538.5	308	263	244.5	228	227	227	227	227	227	227	220	220	207	207	207	207	207	207	200
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Sequence Seq
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2000 2000 2000 2000 1960 1186 11886 11886 11886 11886 11886 11886
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

		and Nucleic
		Polypeptides
SULT 1 -09-907-794A-170 sequence 170, Application US/09907794A Beten No. 6638468 GENERAL INFORMATION: APPLICANT: Generatech, Inc. APPLICANT: Botstein, David APPLICANT: Betsein, Dan L. APPLICANT: Ferrara, Napoleone	Fong, Sherman Gao, Wei-Qiang Gerber, Hanspete Gerricsen, Mary Goddard, A. Goddwski, Paul J Grimaldi, Christ Gurney, Austin L Hillan, Kenneth, Kljavin, Yavr J. Mather, Jennie P Pan, James Pan, James Roy, Margaret An Stewart, Timothy Tumas, Daniel Fundas, Daniel Fundas, Daniel	: Wood, William, I. TWUENTION: Secreted and Transmembrane INVENTION: Acids Encoding the Same RENCE: 10466-11 RENCE: 10466-12 RENCE: 10466-12 RENCE: 10466-12 LICATION NUMBER: US/09/07,794A LICATION NUMBER: US/09/07,794A LICATION NUMBER: US/01/0414 LICATION NUMBER: US/01/13,048 LICATION NUMBER: US/01/146,222 LICATION NUMBER: US/01/146,222 LICATION NUMBER: PS/07-26 LICATION NUMBER: PS/07-28 LICATION NUMBER: PCT/US/99/20594 LICATION NUMBER: PCT/US/99/20594 LICATION NUMBER: PCT/US/99/21090 LICATION NUMBER: PCT/US/99/21090 LICATION NUMBER: PCT/US/99/21090 LICATION NUMBER: PCT/US/99/21090 LING DATE: 1999-09-18 LICATION NUMBER: PCT/US/99/21090 LING DATE: 1999-09-18 LICATION NUMBER: PCT/US/99/21090 LING DATE: 1999-09-15
KESULT 1 US-09-907-794A-170 i Sequence 170, Ap i Patent No. 6635A i GENERAL INFORMAT APPLICANT: Gene APPLICANT: Bot APPLICANT: Bot APPLICANT: Bot APPLICANT: Ext	APPLICANT:	TITLE OF TITLE OF TITLE OF TITLE OF CURRENT AFFE CURRENT AFFE CURRENT AFFE PRIOR FILE PRIOR AFFE
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Godowski, Paul J. Grimaldi, Christopher J.

Goddard, A.

Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E.

Ferrara, Napoleone Filvaroff, Ellen

Ashkenazi, Avi Botstein, David Desnoyers, Luc Baton, Dan L.

Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, Jakes

Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel

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163 LTNNVNKLLIDYSENRLLACGSLYQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTM 222
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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28113
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR PLICATION NUMBER: PCT/US99/28565
PRIOR PLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-02
PRIOR PLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-06
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/30091
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Best Local Similarity 51.6
Matches 269; Conservative
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ORGANISM: Homo sapiens
US-09-907-794A-170
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APPLICANT: Tunnas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and OTHER SETTING OF INVENTION: Secreted and Transmembrane Polypeptides and CURRENT PERIOR TABLES. 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR APPLICATION NUMBER: POT/05/00/0414
PRIOR APPLICATION NUMBER: POT/05/06/0414
PRIOR APPLICATION NUMBER: US/01/05/06/04
PRIOR PLILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-03
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13.5%; Score 1351.5; DB 4; Length 552;
Best Local Similarity 51.6%; Pred. No. 8.4e-113;
Matches 269; Conservative 81; Mismatches 116; Indels 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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8

RESULT 2
US-09-905-125A-170

; Sequence 170, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

SCHOLLANT ACKERATION:
APPLICANT ACKERAT, AVI
APPLICANT ACKERAT, AVI
APPLICANT ACKERAT, AVI
APPLICANT BOCSTELIN, David
APPLICANT EACON, Dan L.
APPLICANT EACON, Dan L.
APPLICANT EACON, Dan L.
APPLICANT EACON, Met-Qiang
APPLICANT FONG, Sherman
APPLICANT Gerber, Hanspeter
APPLICANT Gerber, Hanspeter
APPLICANT Gerber, Amy E.
APPLICANT Gerber, Amy E.
APPLICANT Gerber, Amy E.
APPLICANT Godowski, Paul J.
APPLICANT Granaldi, Christopher J.
APPLICANT Granaldi, Christopher J.
APPLICANT Granaldi, Christopher J.
APPLICANT Hillam, Kenneth, J.
APPLICANT Macher, Jennie P.
APPLICANT Macher, Jennie P.
APPLICANT Paoni, Nicholas F.
APPLICANT FOW, Margaret Ann
APPLICANT Tumas, Daniel
APPLICANT Tumas, Daniel
APPLICANT Tumas, Daniel
APPLICANT Stewart, Timothy A.
APPLICANT Tumas, Daniel
APPLICANT STEWART, Timothy A.
APPLICANT Tumas, Daniel
APPLICANT TUMON Acids Encoding the Same
FILE REFERRNCE: 10466-14
CURRENT FILING DATE: 2001-07-10 287 DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346 406 PSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPG---STTKEQVYTSKLVRLCKE 286 283 PSDILALVSHFDIFYIYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340 LDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGN 466 SRLLT---AAPLSMEQRQPWPRALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHSENRDW 102 FGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKI 229 103 TFNHLIVHQGTGAVYVGAINRVYKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLT 347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG GFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLT 467 ALQYE----TVQVVDPGPVLRDMAFSK-DHEQLYIMSERQ 501 Sequence 170, Application US/09902775A Patent No. 6686451 GENERAL INFORMATION: STLLTROPAPLSOKOR RESULT 3 US-09-902-775A-170 341 515 45 20 170 230 407 23 g & 6 6 6 g 8 a ઠે 염 ò 셤 δ

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FIT MAY 48 10:48:4/ 4004

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283 PSDILALVSHPDIFYIYGFASGGFVYFLTVQPE--TPEGVAINSAGDLFYTSRIVRLCKD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 MKSLDBSALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 TINNVNKWLLIDYKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSV 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 LINNVNKILIIDYSENRILAGGSLYGGVCKLIRIDDEFILVEPSHKKEHYLSSVNKTGIM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSDTFTIIPDFDIXYVYGPSSGNFVYFLTLQPEMVSPPG---STIKEQVYTSKLVRLCKE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.5%; Score 1351.5; DB 4; Length 51.6%; Pred. No. 8.4e-113; ive 81; Mismatches 116; Indels
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 1000-02-22
PRIOR PLING DATE: 1090-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-28
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PRIOR PLING DATE: 1999-11-29
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PRIOR PLING DATE: 1999-12-02
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Best Local Similarity 51.6
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Homo sapiens
US-09-902-775A-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230
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8 6	LDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAVYVKNHSLAFVGTKSGKLKKIRVDGPRGN	qq	: : : 166 VYR-AGRUN
3	401 DDINKEDGGSIEVEGBILDIIISKDKMISVASIVINGISVVEVGIKSGKLKKVKV 514	ò	209 EADGMFAYVI
3 8	ALC TERES	qq	: : 225 LCEGAGSLH1
}	THE ROOMS THE BOOMS TO A WAR IN TAKE IN	ò	268 GSTIKEQVY
RESULT	81-706-2	qq	269 QST
; Segui	Sequence 2, Application US/09181706	ò	327 GVHPDDDLLI
GENI	NERAL INCREMENTION:	ą	303LDVW
	AFFILCANI: MELANIE N. SDINGGB, MICHAEL K. COMEAU, APPLICANT: Robert F. DuBose, Richard S. Johnsonn TITHE OF INTERMITON, VIDAL ENCORDS ESPANDEDEN DECENT	ò	385 W-LKVKDIP
T E E	TITLE OF INVENTION: VICAL ENCODED SEPARTICALN FACIETY TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES MINRER OF SECHENCES: 10	đ	: 345 WDFKTAESH(
 	CORRESPONDENCE: 100	ò	444 SLAFVGTKS
oraginal s	ADDARDORE: OMNES C. MULLY STREET University St.	ପ୍	388 TVLFLGTGD
	CIII: SERVITE CINTE: WA CONNED. II	ò	491 HEQLYIMSE
	COUNTY OF STORY OF ST	qa	436 NIYIYLTAG
	MEDIUM TYPE: Flopy disk	ò	551 FASEMKQCV
na ea e	COMPANIES IDN FC COMPANIES OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS	qa	488
ぢ 、、、	SOCIATION APPLICATION DATA: ADDITORATION NUMBER: 11.0, VEIBION #1.30	ò	611 QCYSPAAKE
sammi-bi	AFFILENTION NUMBER: US/US/121,/US FILING OCTOBER 28, 1998	ପ୍ର	503AKK
E .		λō	670 YRCHWCKYR
	APPLICATION NUMBER: US 08/958,598 (Converted to a APPLICATION NUMBER: Provisional, see below)	qa	543R
	CLASSIFICATION COCCUER 20, 133/ CLASSIFICATION DATA.	ò	730 POSGORGYE
	APPLICATION NUMBER:to be assigned (USSN 08/958,598 APPLICATION NUMBER: conversion to Drawisional annication)	q _Q) 552 PNRT
2000g - 1 g	FILING DATE: October 26, 1998 CLASSIFICATION:	λο ·	788 HFNIDNPAQI
,	ATTORNEY/AGENT INFORMATION: NAME: Henry Janis C	qq	586 RFNFTN
	REGISTRATION NUMBER: 34,347 REFERENCE/DOCKET UNMBER: 2611-a	<i>λ</i> ο	848 LSGAKSKCTI
Ε΄	TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 470-4189	qu	
· INF	2	ò	908 YIPABQIVC
σο · · · · · · · · · · · · · · · · · · ·	TERISTICS:	q _C	626 DYERNÇEQC
e no opi	TYPE: amino acid TOPOLOGY: linear	ò	962 SRGPMSGGT
M . US-09-	; MOLECULE TYPE: protein US-09-181-706-2	qq	670 QKVSTLGKSI
Quer	13.5%;	ò	1015 LEMK-VSVQ
Best Matc		đ	
<i>λ</i> δ	VTHETGPDEDNPKCYPPRIVQTCNBPLTTNNVNKM	λö	
QQ O	70 YSLEHSLSRLYRDQAGNCTEPVSLAPPARPRGSSFSK-LLLPYR 113	දුය	IISH
ò	124 ENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSVFGV 172	<i>λ</i> δ	1134 TNFT
Q Q	114 EGAAGLGGLLLTGWTFDRGACEVRPLGNLSRNSLRNGTBVVSCHPQGSTAGV 165	qa	831 TYLDCGTLO
\ \ \ \ \	173 IVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNS 208	∂	1189 PCTVTV
o production			

166	: :::::; : VYR-AGRNNRWYLAVAATYVLPEPETASRCNPAASDHDTAIALKDTEGRSLATQELGRLK 224
209	BADGMFAXVFHDEFV-ASMIKIPSDTFTIIPDFDIXYVYGFSSGNFVYFLTLQPEMVSPP 267
268 269	GSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVE-YRLLQAAYLSKAGAVLGRTL 326
327	GVHPDDDLLPTVFSKGQKRKMKSL : : :: LDVWAGVFSAAAGEGQERRSP
385 345	W-LKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVKNH 443
444 388	SLAFVGTKSGKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKD 490 :: :
491	HEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRR 550 : : : : : : : :
551	FASEMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQI 610
611 503	QCYSPAAKEVPRIITENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCL-SCVESP 669
670	YRCHWCKYRHVCTHDPKTCSFQBGRVKLPBDCPQLLRVDKILVPVBVIKPITLKAKNLPQ 729
730	POSGQRGYECILNIQGSEQRVFALRFNSSSVQCQNTSYSYBGMEINNLFVELTVVWNG 787
788 586	HFNIDNPAQNKVHLYKCGAMRB
848	LSGAKSKCINPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDG 907
908	YIPAEQIVCEMGEAKESQHAGFVEICVAVCRPEFMARSSQLYYFWTLTLSDLKP 961
962	SRGPMSGGTQVTITGTNLNAGSNV-VVMFGKQPCLFHRRSPSYIVCNTTSSDEV 1014 :
1015	LEMK-VSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQI 1073
1074	RAKHGGKEHINICEVLNATEMTCQAPALALGFDHQSDLTERPEEFGFILDNVQSLLILNK 1133
1134	TNFTYYPNPVFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVXLNYTVLVGEK 1188
1189	PCTVTVSDVQLLCESPNLIGRHKVMARVGGMEYS 1222

Db 876 DIEITLFHGENGQLNCSFENITRNQDLTTILCKIKGIKTASTIANSSKKVRVKLGNLE 933	; APPLICATION NUMBER: US/09/4:	9/458,791
QY 1223 PGWVYIAPDS-PLSLPAIVSIAVAGGLLIFIVAVLIAYKRKSRESDLTLKRLQMQMDNL 1281	HzZ	58,598
Qy 1282 BSRVALECKEAFAELQTDIHELTS	; FILING DATE: 2B-OCT-1997 ; ATTORNEY/AGENT INFORMATION: ; NAME: Henry, Janis C ; REGISTRATION NUMBER: 34,34	
QY 1339 EVPGYRQERUEKGLKLFA-QLINNKVFLLSFIRTLESQRSFSMRDRGNVASLIMTVLGS 1396 1042HNRDANDKOHSLTALDALICNKSFLVTVIHTLEKQKNFSVKDRCLFASFLTIALQT 1097	ENCE/DOCKET NUMBER: ICATION INFORMATION: HONE: (206)470-4189 AX: (206)233-0644	2631 :
QY 1397 KLEYATDVLKQLLADLIDKQNLESKAHPKLLLRRTESVAEKMLTNWFTPLLYKPLKECAGE 1456 DD 1098 KLVYLTSILEVLTRDLMEQCSNMQPKLMLRRTESVVEKLLTNWMSVCLSGFLRETVGE 1155	; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 1569 amino acids ; TYPE: amino acid	
QY 1457 PLFSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDXKTLVLSCVSPDNANSP 1513	/ TOPOLOGY: linear // MOLECULE TYPE: protein // SEQUENCE DESCRIPTION: SEQ ID NO	NO: 2:
OY 1514EVPUKILNCDTITQVKEKILDAIFKQVPCSHRPKAADMDLEWRQGSGARMILQDEDI 1570	13.5%; Scc larity 24.8%; Pre Jonservative 291;	Score 1349; DB 3; Pred. No. 1e-111; ; Mismatches 591
QY 1571 TTKIENDWRRLNTLAHYQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYENMIRYTGS 1630 1276 SVILEDGITKLNTIGHYEISNGSTIKVFKKIANFTSD 1312	Qy 72 YKLSSDLKVLVTHETGPDEDNPKCXPPRIVQTCNEPLI 	YPPRIVQTCNEPLT ::
QY 1631 PDSLRSRTPMITPDLESGVKWHHLVKNHEHGDQKEGDRGSKMVSEIYLTRLLATKGTL 1688 1313 VEYSDDHCHLILPDSEAFQDVQGKRHRGKHKFKVKEMYLTKLLSTKVAI 1361	Qy 124 ENRLIACGSLYQGICKLLRLEDLFKLGEPYHW	RLEDLFKLGEPYHY : PLGNLS
QY 1689 QKFVDDLFETIFSTAHRGSALFLAIKYMEDFLDEQADKHGIHDPHVRHTWKSNCLFLRFW 1748 1362 HSVLEKLFRSIWSLPNSRAPFAIKYFFDFLDAQAENKKITDPDVVHIWKINSLFLRFW 1419	CY 173 IVSYSNLDDKLFIA	PETASRCNPAASDHI
OY 1749 VNMIKNPOPVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYK 1808	Qy 209 BADGMFAYVFHDEFV-ASMIKIPSDTFTIIPDFDIYYY 1 1 1 1 1 1 1 1 1	DTFTIIPDFDIYYY
OY 1809 NWVERYYSDIGKMPAISDQDMNAYLAEQSRMHNNEFWIMSALSEIFSYVGKYSEEILGPL 1868	Qy 268 GSTTKEQUYTSKLURLCKEDTAFNSYVEVPIGCERSGN Db 269 QSTBVLFQGQASLDCGHGHI	KEDTAFNSYVEVPIGCERSGV : ' EVLFQGQASLDCGHGHE
Oy 1869 DHDDQCGKQKLAYKL 1883 Db 1540 ERERGLEEAQKQLLHVKV 1557	Qy 327 GVHPDDDLLFTVPSKGGKRKMKSLDESALCIFILKK : : : :	CSLDESALCIFILK(: : : SPTTTALCLFRMSE
RESULT 5 US-09-458-	Qy 385 W-LKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRC	.DMNAPLGVSDMVRC : : : DQPERVQI
<pre>// Sequence 2, Application US/09458791 // Patent No. 6174689 // GENERAL INFORMATION: // APPLICANT: Spriggs, Melanie</pre>	QY 444 SLAFVGTKSGKLKKIRVDGPRGNALQYETVQVV	GPRGNALQYETVQVV
TITLE ; HUMBE ; CORRE	Qy 491 HEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCC : : : : :	SCGECLGSGDPHCC
14 14 14 ·	551	WLLVLETYNVPELS
SIGNIE: WA COUNTRY: US ZIP: 98101	DD 488NWLDIN OY 611 QCYSPAAKEVPRIITENCDHHVVQLQLKSKEIGMTFAK	OLOLKSKETGMTFA:
	503	
OPERATING SYSTEM: MS-DOS/Windows 95 SOFTWARE: Word for Windows 95, 7.0a CURRENT APPLICATION DATA:	Qy 670 YRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLR?	SRVKLPEDCPQLLR

	D W C		
; ; ; US-09-458	4		
Query M Best Lo Matches	ery Match st Local Similarity 24.8%; Pred. No. 1e-111; tches 480; Conservative 291; Mismatches 591; Indel	n 1568; .s 576; Gaps	74;
à	72 YKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTT	MLLIDYK	123
Db	70 YSLEHSLSRLYRDQAGNCTEPVSLAPPARPRPGSSFSK	LLLPYR	113
ò	124 ENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGV	NESGSVFGV	172
Db	114 EGAAGLGGLLLTGWTFDRGACEVRPLGNLSRNSLRNC	SRNSLRNGTEVVSCHPQGSTAGV	165
ò	173 IVSYSNLDDKLFIATAVDGKE	-TAVDGKPEYFPTISSRKLTKNS	208
qq	166 YYR-AGRUNRWYLAVAATYVLPEPETASRCNPAASDHDTAIALKDTEGRSLATQELGRLK		224
ò	209 BADGMFAYVFHDEFV-ASMIKIPSDIFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSP	α	267
QQ	225 LCEGAGSLHFVDAFLMNGSIYFPYYPYNYTSG	AATGWPSMARIA	268
ò	268 GSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVE-YRLLQAAYLSKAGAVLGRTL		326
Db	269 QSTBVLFQGQASLDCGHGHPDGRRLLLSSSLVEA		302
ờ	327 GVHPDDDLLFTVPSKGQKRKNKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLA		384
d d	303LDVWAGVFSAAAGEGQERRSPTTTALCLFRMSEIQARAKR	. sa	344
λŏ	385 W-LKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYYKNH		443
Ωp	345 WDFKTAESHCKEGDQPERVQPIASSTL	ERVQPIASSTLIHSDLTSVYGTVVMNR	387
ò	444 SLAFVGTKSGKLKKIRVDGPRGNALQYETVQVV	-DPGPVLRDMAFSKD	490
qq	388 TVLFLGTGDGQLLKV1LGENLTSNCPEVIYEIKEETPVFXKLVPDPV	K	435
ò	491 HEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRR		550
qq	436 NIXIYLTAGKEVRRIRVANCNKHKSCSECLTAIDPHCGWCHSLQRCTFQGDC		487
ò	551 FASEMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQI		610
QQ	488VHSENLENWLDISSG		502
ò	611 QCYSPAAKEVPRIITENGDHHVVQLQLKSKETGWIFASTSFVFYNCSVHNSCL-SCVES	Д	699
q	503AKKCPKIQIIRSSKEKTTVTMVGSF	-SPRHSKCMVKNVDSS	542
č	670 YRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNLPQ		729
qq	543RELC	ÖSWKSÖ	551

		. ~	
209 EADGMFAYV	HSVLEKLFRSIWSLPNSRAPFAIKYFFDFLDAQAENKKITDPDVVHIWKTNSLPLKFW 1419 Qy	Db 1362 HS	
166 VYR-AGRNN	1748	1689	
173	1361	Db 1313 VE	
114	GVKWWHLVKNHEHGDQKEGDRGSKMVSEIYLTRLLATKGTL 1688	1631	
124	SVILEDGITKLNTIGHYEISNGSTIKVFKKIANFTSD 1312	Db 1276 SV:	Service Comments
70	VSKQVTAYNAVNNSTVSRTSASKYENMIRYTGS 1630	Oy 1571 TT	
72 YKL	DTIGGAKEKIFQAFLSKNGSPYGLQLNEIGLELQMGTRQKELLDIDSS 1275	Db 1216 VC	
Query Maccii Best Local Similarity Matches 480; Conser	EVPVKILNCDTITQVKEKILDAIFKAVPCSHRPKAADMDLEWRQGSGARMILQDEDI 1570 Gest Best	Qy 1514	نس يالوه
-09-459-066-Z	: :: EKIPENESAD 1215	1156	a Lagran
; TOPOLOGY: linea; pr	SKGPIDALTGEARYSLSEDKLIRQQIDYKTLVLSCVSPDNANSP 1513	Qy 1457 PL	
568 mir	1155	 Db 1098 KLN	
SEQUENCE CHARACTER	1456	Qy 1397 KLI	
TELEFACNE: (205 TELEFAX: (206)2	::::	Db 1042	
TELECOMMUNICATION	1396	Qy 1339 EVE	
ATTORNEY/AGENT INF NAME: Henry, Ja REGISTRATION NUM	ESRVALECKEAFAELQTDIHELTSDLDGAG-IPFLDYRTYTWRVLFPGIEDHPVLRDL 1338 ; A'	Qy 1282 ESF 	
APPLICATION NUMB	LYVEQESUPSTWYFILVLDPVLLVIVIFAAVGVTRHKSKELSRKQSQ-QLELL 984	Db 934	
CLASSIFICATION:	FIVAVLIAYKRKSRESDLTLKRLQMQMDNL 1281	Qy 1223 PGN	
CURRENT APPLICATION NUMB		876	
OPERATING SYSTEM SOFTWARE: Word	GRHKUMARVGONFYS 1222	, r	
COMPUTER READABLE MEDIUM TYPE: FL COMPUTER: IBM P	TNFTYYPNVPEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVYKLNYTVIVGEK 1188 ; CC	Oy 1134 T Db 831 TYI	
COUNTRY: US ZIP: 98101	830	Db 786 IIS	
CITY: Seattle STATE: WA	RAKHGGKEHINICEVINATEMTCQAPALALGPDHQSDLTERPESFGFILDNVQSLLILNK 1133	Qy 1074 RAK	
ADDRESSEE: Jani	-BMXDVCIQEDGGNCSSVGSLSYIALPHCSLIFPATTWISGGQNITWMGRNFDVIDNL 785	11 DD 729 - EM	
NUMBER OF INVENTION NUMBER OF SEQUENCE	LEMK-VSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQI 1073	Qy 1015 LEN	
APPLICANT: Spring TITLE OF INVENTION	: :	; Db 670 QKV	
GENERAL INFORMATION:	SRGPMSGGTQVTITGTNLNAGSNV-VVMFGKQPCLFHRRSPSYIVCNTTSSDEV 1014 ; GENI	Qy 962 SRG	
US-09-459-066-2; Sequence 2, Applicati	6 99		
E	IHPFTAS 625	616	
ERER	LSGAKSKCTNPRITEIIPVIGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDG 907	Qy 848 LSG	
		Db 586 RFNFTN	
TROS NAVERYKED.	GY HENIDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPGQCTLRQHCPAQESQWLB 847	Qy 788 HFN	
	585	552	
	POSGORGYECILNIQGSEORVPALRFNSSSVQCQNTSYSYEGMEINNLPVELTVVWNG 787	Qy 730 PQS	

Qy 17 Qy 18 Qy 18 Db 19 Qy 18 RESULT 6 US-00-459-(1749 VNMIKNPQFVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSFSNKLITAKOIPSYK 18 1420 VNILKNPQFVFDIKKTPHIDGCLSVIAQTFMDSCSTSEHRLGKDSFSNKLITAKAIPTYK 14 1420 VNILKNPQFVFDIKKTPHIDGCLSVIAQAFMDAFSLTEQQLGKEAPTNKLIYAKDIPTYK 14 1809 MVERYYSDIGKMPALSDQDWAYALAEQSRAHMABFNTMALSEITSYVGKYSEEILGPI 18 1480 EEVKSYYKAIRDLPPLSSSEMEFLTQESKKHENEFNEEVALTEIYKYIVKYFDEILNKL 15 1869 DHDDQCGKQKLAYKL 1883 1540 ERERGLEEAQKQLHVKV 1557 1540 ERERGLEEAQKQLHVKV 1557 6 6 6 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7	108 179 188 188 188 188 188 188 188 188 188 18
Paten GANE TIT TIT TIT COO	GENERAL INFORMATION: APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie APPLICANT: Spriggs, Melanie TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEB: Janis C. Henry STREET: 51 University St. CITY: Seattle STATE: WA COUNTRY: US ZIF: 98101 COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IRA PC Compatible COMPUTER: IRA PC Compatible COMPUTER: MS-DOS/Windows 95 SOFTWARE: Word for Windows 95, 7.0a	
PRR AT TE SE	CURRENT APPLICATION DATA: APPLICATION MUMBER: US/09/459,066 FILING DATE: CLASSIFICATION PRIOR APPLICATION APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/958,598 FILING DATE: TILING DATE: APPLICATION NUMBER: 34,347 REGISTRATION NUMBER: 34,347 REGISTRATION NUMBER: 34,347 REGISTRATION NUMBER: 34,347 REGISTRATION NUMBER: 2631 TELECHONE: (206)233-0644 TELECHONE: (206)233-0644 SECURIC CHARACTERISTICS: LENGTH: 1568 amino acids TOPE: Accesin	
Query Ma Best Loc Matches	<pre>itch 13.5%; Score 1349; DB 3; Length 1568; ial Similarity 24.8%; Pred. No. 1e-111; 480; Conservative 291; Mismatches 591; Indels 576; Gaps</pre>	74;
B &	72 YKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLITTNNVNKMLLIDYK 12 	23
<u>8</u> 5	124 ENRLIACGSLYQQICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSVFGV 17:	72
දු පු	173 IVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNS 20 : : : :	0 8 4 4
ζ	209 EADGMFAYVFHDEFV-ASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPP 20	193

us-09-964-956-13.rai

74; 435 487 FASEMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQI 610 699 542 729 787 444 SLAFVGTKSGKLKKIRVDGPRGNALQYETVQVV------DPGPVLRDMAFSKD 490 : | : | : | 302 ------EVLFQG--QASLDCGHGHPDGRRLLLSSSLVEA------ 302 W-LKVKDIPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNH 443 72 YKLSSDLKVLVTHETGPDEDNPKCYPPRIVOTCNEPLTTT------NNVNKALLIDYK 123 GSTTKEQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVE-YRLLQAAYLSKAGAVLGRTL 326 GVHPDDDLLFTVFS--KGOKRKWKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLA 384 QCYSPAAKEVPRIITENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCL-SCVESP YRCHWCKYRHVCTHDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVEVIKPITLKAKNLPQ POSGORGYECILNIQGSEORVPALRFNSSSVQCQNTSYSYEGMEINNLPVELTVVWN--G PNR-----TCTCSI-----PTRATYKDVSVVNVMFSFGS-------WNLSD WDFKTAESHCKEG-----DQP----ERVQPIASSTLIHSDLTSVYGTVVMNR HEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRR EADGMFAYVFHDEFV-ASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPP -----NMTDISSG-------ENR-----LIACGSLYQGICKLIRLEDIFKLGEPYHKKEHYLSGV----NESGSVFGV Gaps Query Match
13.5%; Score 1349; DB 4; Length 1568;
Best Local Similarity 24.8%; Pred. No. 1e-111;
Matches 480; Conservative 291; Mismatches 591; Indels 576; ATTORNEY DATE:
ATTORNEY AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acids
TYPE: amino acids APPLICATION NUMBER: 08/958,598 ------VHSENLE--TOPOLOGY: linear MOLECULE TYPE: protein US-09-459-065-2 551 611 20 124 173 166 327 345 388 491 488 503 114 509 225 268 303 385 269 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 g a DB 8 8

ESRVALECKEAFAELOTDIHELTSDLDGAG-IPFLDYRTYTWRVLFP--GIEDHPVLRDL 1338 1041 1396 1097 KLEYATDVLKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTFLLYKFLKECAGE 1456 1513 1215 1570 1275 1688 1361 1748 1419 1808 NWVERYYSDIGKMPAISDQDMNAYLAEQSRMHANNEFNTMSALSEIFSYVGKYSEEILGPL 1868 1281 1188 875 961 HFNIDNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCQGPGQCTLRQHCPAQESQWLB 847 PLFSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLSCV---SPDNANSP SEYSDDHCHLILPDSEA----FQDVQGKRH------RGKHKFKVKEMYLTKLLSTKVAI VNMIKNPOFVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYK TTKI ENDWKRLNTLAHYQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYENMIRYTGS .074 RAKHGGKEHINICEVLNATEMTCQAPALALGPDHQSDLTERPEBFGFILDNVQSLLILNK | : | : | | | | | : : : | | | | : : : | | ESELRKEIRDERDYKHFALRIFFPESGGFTHIFTEDM SVILEDGITKINTIGHYEISNGSTIKV-------FKKIANFISD PDSLRSRTPMITPDLESGVKWWHLVKNHEHGDQKEGDRGSK--MVSEIYLTRLLATKGTL OKEVDDLFETIFSTAHRGSALFLAIKYMFDFLDEQADKHGIHDPHVRHTWKSNCLFLRFW 729 -EMKDVCIQFDGGNCSSVGSLSYIALPHCSLIFFATTWISGGQNITMMGRNFDVIDN--L -----GRHKVMARVGGMEYS 223 PGMVYIAPDS-PLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSRESDLTLKRLQMQMDNL EVPGYROERVEKGLKLFA--QLINNKVFLLSFIRTLESORSFSWRDRGNVASLIMTVLOS LSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDG 908 YIPAEQIVÇEM-----GEAKPSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKP DYERNOEQCPVAVEKTSGGGRPKENKG-----NRTNQALQVFY----IKSIEP SRGPMSGGTQVTITGTNLNAGSNV-VVMFGKQPC-----LFHRRSPSYIVCNTTSSDEV 670 QKVSTLGKSNVIVTGANFTRASNITMILKGTSTCDKDVIQVSHVLNDTHMKFSLPSSRK-1015 LEMK-VSVQVDRAKIHQDLVFQYVEDPTIVRIEPEWSIVSGNTPIAVWGTHLDLIQNPQI 786 IISHELKGNINVSEYCVATYCGFLAPSL------KSSKVRTNVTVKLRVQD 1134 T----NFTYYPNPVFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEK ---EVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAADMDLEWROGSGARMILQDEDI 1189 PCTVTV---SDVQLLCESPNLI-------------iHPFTA------RFNFTN 1282 985 1339 1042 1397 1098 1457 1514 1571 1631 1689 831 934 616 929 요 g 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 ठ हे ठ ઠ ద ò g ઠ 염 8

Db 1480 EEVKSYYRAIRDLPPLSSSEMEEFLTQESKKHENEFNEEVALTEIYKYIVKYFDEILNKL	1539	OY 622 RIITENGDHHVVQLQLKSKETGMTFASTSFVFXNCSVHNSCLSC
Qy 1869 DHDDQCGKQKLAYKL 1883		Db 469 QMVLQRSSSYVVALTNF
Db 1540 ERERGLEEAQKQLLHVKV 1557		Qy 682 THDPKTCSFQEGRVKLPEDCPQLLRVDKILVPVBVIKPITLKAK
e E E E E E E E E E E E E E E E E E E E		Db 486
US-09-145-473E-24 ; Sequence 24, Application US/09345473E		742 NIQGSEQR
		506
artin No. 6558903el Kina 00/183781		OY 802 YKCGAMRESCGLIXADPRACGWGGGGGGGGTLRQHCPAQEEGW DD 527TCDRCLRAERFWGGGWC-GNG-CTRHHECAGFW
		Qy 862 EIIPVTGPREGGTKVTIRGENLGLEFRDIASH
		DD 568 DFHPRSAPLRGQTRVTLCGMTFHSPPDFTAHHSLPGPYRV
; SEQ 1D NO 24 ; TWOR: 1404 ; TWOR: PRT		QY 908 YIPABQIVCEMGEAKPSQHAGFVEICVAVCRPEFM
; ORGANISM: Gallus gallus US-09-345-472E-24		DD 624 YRPLPTFRRKDFVDVLVCVLBPGBPAVAÄGPADVVLNVTESAGT
5.4%; Score 538.5; DB 4;	Length 1404;	QY 952 MILILSDLKPSRGPMSGGTQVTIIGTNLNAGSNVVVMFGKQPCL
223; Mismatches 548;	Indels 599; Gaps 78;	1008
10 CLLSHLLMVGMGSSTLLTRQPAPLS : : : : :	58	743
ហ	28	Qy 1068 IQNPOJRAKHGGKEHINIÇEVLNATE-MTÇQAPALALGPDHQ
Cy S9 RTGHIYLGAVNRIYKLSSDLKVLVTHETG9DEDNPKCYPPRIVQTCNBPLTTTNNVNRML 	118	Db 801 VYRAKIQFQGGGGGKTBATECEGPQSPNWLLCRSPAFPI
119	164	1125
Db 118 LLDPVEPWLYSCGTARRGLCYLHQLDVRGSEVTIASTRCLYSAAANSPVNCPDCVASPLG	177	
Qy 165 ESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFP-TISSRKLTKN ::: : :: : : :	PEYPP-TISSRKLTKNSEADGWPAYVFHDE 221	OY 1184 LOGER-CITTYSDVQLLCES-RULLCREANING OCHETS OF THE PARTY OCHETS OCHETS OF THE PARTY OCHETS OCHETS OCHETS OF THE PARTY OCHETS OCH
178 STATVVADRYTASFYLG	- 227	Qy 1240 VSIAVAGGLLIIFIVAVLIAYK-RKSR
QY 222 FVASMIKIPSDIFTIIPDFDIXYVYGFSSGNFVYFLTLQPEMVSPFGSTTKEQVYT D	SPPGSTTKEQVYT 277	996
278 SKLVRLCKEDTAFNSYVEVPIGCERSGVE	LLOAAYLSKAGAV 321	OY 1282 ESRVALECKEAFAELQTDIHELTSDLDGAGIPFL
Db 270 TRLVRLSAHEPELRRYREIVLDCRYESKRRRRRRGAEEETERDVAYNVLQAAHAARPGAR	329	1319
322 LGRTLGVHPDDDLLFTVFSKGQKRKMKSLD	381	- : 1082 IPEERLITHRSRVIGRGHFG
330 LARDLGIDGTETVLFGAFAESHPESRAPQH	382	Qy 1349EKGLKLFAQLINNKVFLLSFIRTLE
QY 382 DLAMLKVXDIPCSSALLTIDDNFCGLDMNAPLGVSDMNRGIPVFTEDRI Dh 383	ORMISVIAYVK 441	Db 1142 MKSFHHPQVLSLLGVCLPRHGLPLVVLPYMRHGDLRHFIRAQEF
442 NHSLAFVGTKSGKLKKIRVDGPRGNALOYE		Qy 1374SQRSFSWRDRGNVASLIMTVLQSKLEYATDVL-KQI
404 PHS		1202
Qy 502 LTRVPVBSCGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRFASEMKQCVRL	ERSKEPRRFASEMKQCVRL 561	OY 1425 LLLRRTESVAEKMLINW-FIFLLYKFLKELAGEFLFSH DA 1966 LDIRRTESVAEKMLIN
Db 422 PTLVPAASHHH	KV 432	
562 TVHPNNISVSQXNVLLVLETYNVPELSAGV		
Db 433 DLFNGRLSGTLLTSIFVTVLONVTVAHLGTAOGRVL-	3RVL468	

622	RIITENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYRHVC 681 :::
682	PQLLRVDKILVPVEVIKPITLKAKNLPQPQSGQRGYECIL 74
486	NIOGSBORVDALRENSSSVOCONTSYSYEGMEINNLPVE
506	FAAGTKVWRVNVTGPGCR
802	SGAKSKCTNPRIT 8
527	NG-CTRHHECAGPWVQDSCP-PVLT 56
862 568	BIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDG 907 : : : : : : DFHPRSAPLRGQTRVTLCGMTFHSPPDPTAHHSLPGPYRVAVGGRSCTVLLDESES 623
908	YIPABQIVCEMGEAKPSQHAGFVEICVAVCRPEFMARSSQLYYF 951
952	MILILSDLKPSRGPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVCN 10
684	: :
1008	TISSDEVLEMKVSVQVDRAKIHQDLVFQYVBDPTIVRIEPEWSIVSGNTPIAVWGTHLDL 1067 ::: :: APAATSLGAAPVALWIDGEBFLAPLPPEYRPDPSVLTVVPNCSYGGSTLTLIGTHLDS 800
1068	
1125	VQSLLILNKTNFTYYPNPVFEAFGPSG-ILELKPGTPIILKGKNLIPPVAGGN
855	
1184	LVGEKPCTVTVSDVQLLCESPNLIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAI 1239
1240	VSIAVAGGLLIIFIVAVLIAYK-RKSR
996	
1282	
02	EVQV-LPVADSPGLARPHAHFASAGADAAGGSEVFLLKIISCCLEDLKFELLEEVALL
 1319	TYTMRVLFPGIEDHPVLRDL
1349	
1142	MKSFHHPQVLSLLGVCLP
1374	SQRSFSWRDRGNVASLIMTVLQSKLEYATDVL-KQLLADLIDKNLESKWHPK 1424
1202	
1425	LILRRIESVAEKNLTNW-FTFLLYKFLKECAGEPLFSLFCAIKOOMEKGPIDAI 1477
 14.00	TO BY DOUGH TO COUNTY TO COUNTY TO THE TOTAL OF THE TOTAL
 1304	TGEAKZULSEDALIKQQIDIKILVLSCVSFDNANSF 151ARYLLKGRRLPQPQPCPDTLYGVMLSCWAPTPEERP 133

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Sequence 4, Application US/08556422A

Sequence 4, Application US/08556422A

Patent No. 6576754

GENERAL INFORMATION:

APPLICANT: HALL, Kathryn T.

APPLICANT: SCHULTES, Vaschim L.

APPLICANT: SCHULTES, Vaschim L.

APPLICANT: BOUSSIOTIS, Vassiliki

APPLICANT: BOUSSIOTIS, Vassiliki

APPLICANT: WALLER, Lee M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES

FILE REFERENCE: DFN-005CPA2

CURRENT APPLICATION NUMBER: US/08/556,422A

CURRENT FILING DATE: 1995-11-09

NUMBER OF SEQ ID NOS: 7

SOCTWARR: FASISEQ FOR WINGOWS Version 4.0

SEQ ID NO 4.0

SEQ ID NO 4.0
.08-556-422A-4
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Gaps Query Match
3.1%; Score 308; DB 4; Length 607;
Best Local Similarity 21.5%; Pred. No. 2.4e-18;
Matches 144; Conservative 110; Mismatches 257; Indels 160;

TYPE: PRT
ORGANISM: Mus musculus
US-08-556-422A-4

357 SSLQLPDRVLNFLKDHFLMDGQVRSRLLLLQPRARYQRVAVHRVPGLHSTYDVLFLGTGD 416 535 VPGKPCKQVQIQPNITVNTLACPLLSNLATRLWVHNGAPVNASASCRV--LPTGDLLLLVGS 592 145 196 F------PIISSRKLTKNSBADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYY 244 245 VYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKEDTA------FNSYVEV 296 297 PIGCER--SGVEYRLLQAAYLSKAGAVLGRTLGVHPDD----DLLFTVFSKGQKRKMKSLD 351 352 ESALCIFILKQINDRIKERLQSCYRGEGTLDLAW-LKVKDIPCSSALLTIDDNFCGLDMN 410 411 APLGVSD-----VYKNHSLAFVGTPVFTEDRDRMTSVIAY----VYKNHSLAFVGTKS 452 453 GKLKKIRVDGPRGNALQYETVQVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCGQ 512 513 YOSCGECLGSGDPHCGW----CVLHNT-------CTRXERCERSKEPRRFA 552 553 SEMKQCVRLTVHPNNISVSQYNVLLVLET----YNVPELSAGVNCTFEDLSEMDGLVVGN 608 DRK-----QQCSFKGKDPKRDCQNYIKILL-PINSSHLLTCGTAAFSPLCAYIHIAS 36 KORSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVTHE-----TGPDE 91 DNPKCYPPRIVOTCN----EPLITINNVNKMLLIDYKENRLIACG-SLYQGICKLLRLED 146 LFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLD-----DKLFIATA--VDGKPEY Q-----IQCYS 614 61 oy oy g ò 8 8 8 S q

593 QQGLGVFQCWS 603

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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Methods and Maaterials Relating to Semaphorin-Like
TITLE OF INVENTION: Polypeptides and Polynucleotides
FILE REFERENCE: HYS-23
CURRENT APPLICATION NUMBER: US/09/653,274
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 13
SSG ID NO 4
LENGTH: 1086
                                                                                                                                                                                        TYPE: PRT
, ORGANISM: Homo sapiens
US-09-653-274-4
                                                                                                                                                                                                                                                                                                                                                                                                                                     123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SD-----YKNHSLAFVGTKS 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 GTVLKPLVKPNASVSGTTGPSIFLEEFETYRPDRCGRSSSAGEWGORLLSLELDAASGGL 512
                                                                                                                                                                                                                                                                                                                                62 GAEDLNIQRVLRVNRT--LFIGDRDNLYQVELEPSTSTELRYQRKLTWRSNPSD----- 113
                                                                                                                                                                                                                                                                                                                                                                    97 PPRIVQTC----NEPLITINNVNYMALLIDYKENRLIACGS-LYQGICKLIRLEDLFKLGE 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPPTISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 INDRIKERLOSCYRGEGTLDLAWLKVKD--IP----CSSALLTIDDNFCGLDMNAPLGV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKLKKI-----RVDGPRGNALOYETVQVVDP------GPVLRDMAFSKDHEQL 494
                                                                                                                                                                                                                                                                                                                                                                                                                        -----PYHKKEHYLSGVNESGSVFGVIVS-----YSNLDDKLFIATAVDGKPE 194
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                                                                                                                                                                                                                                                                            50 GFNHLVVD-----ERTGHIYLGAVNRIYKL-----SSDLKV--LVTHETGPDEDNPKCY
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                                                                                                                                                                                                                                   Gaps
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2.4%; Score 244.5; DB 4; Length 887;
Best Local Similarity 22.2%; Pred. No. 2.7e-12;
Matches 141; Conservative 86; Mismatches 206; Indels 203;
 Patent No. 6576441
GENERAL INFORMATION:
APPLICANT: KIMURA, TOTU et al.
TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE STILE REFERENCE: 0020-4426P
CURRENT APPLICATION NUMBER: US/09/077,940A
CURRENT FILING DATE: .1998-06-05
NUMBER OF SEQ ID NOS: 20
SOFTWARR: Patentin version 3.1
SEQ ID NO 2
LENGTH: 887
                                                                                                                                                                                                                                                             8 WT-----CLLSHLLMVGMGSSTLLTROPAPLSOKORSFVTF---
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US-09-077-940A-2
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US-09-653-274-4
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D--RDRMTSV----IAYVYKNHSLAFVGTKSGKLKKI--------RVDG 462
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                                                                                                                                                                                                                                                                                                                                  RLCKEDTA------FNSYVEVPIGCERSG-----VEYRLLOAAYLSKAGAVLGRT 325
                                                                                                                                                                                                                                   164 --NESGSVFGVIVSYSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                      FVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 YDSKWIKEP-------HFLHAIEYGNYVYFFFRE--IAVEHNNLGKAVY-SRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 LGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 LKVKD--IP-----CSSALL-----TID--DNFCGLDMNAPLGVSDM--VRGIPVFTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GHIYLGAVNRIYKLSSDLKVLVTHETGPD------BDNPKC-YPPRIVQTCNEPLIT
                                                                                                                                                                                                                                                                                                     111 TNNVNKMLLIDYKENRLIACG-SLYQGICKLLRLEDLFKLGEPYHKKEHYLSGV-----
                                                                                                      10 CLLSHLLMVGMGSSTLLTRQPAPLS----QKQRSFVTFRGEPAEGFNHLVVD----ERT
                                                       Indels 168;
Query Match
2.3%; Score 228; DB 4; Length 1086;
Best Local Similarity 19.9%; Pred. No. 1.2e-10;
Matches 123; Conservative 107; Mismatches 219; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08121713D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application US/08; Patent No. 2639866; GENERAL INFORMATION: APPLICANT: Goodman, Corey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-121-713D-62
```

Sequence 4, Application US/09653274
PRETENT NO. 6655742
GENERAL INFORMATION:
APPLICANT: Boyle, Bryan J
APPLICANT: Yeung, George X
APPLICANT: Yeung, George X
APPLICANT: Mize, Nancy K

385

```
------CSYNITVDAHRCTPPNKSNDYQ 676
                                                                        471 ETVQVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCG-QYQSCGECLGSGDPHCGW
                                                                                                                                                           530 CVLHNTCTRKER------CERSKEPRRFASEMKOCVRLTVHPNNISVSQYNVL
                                                                                                                                                                                                                                                                                                 577 LVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      637 LKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYR----HVCTHDPKTCSFQ
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2.3%; Score 227; DB 1; Length 724;
Best Local Similarity 20.4%; Pred. No. 6.9e-11;
Matches 147; Conservative 118; Mismatches 260; Indels 196;
                                                                                                                                                                                                                            544 DKEANTCRPYELDLLQDVANETSDICDSSVLKKKIVVTYGQSVHLGCF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goodman, Corey S.
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US/08/835,268
FILING DATE: IS SEP-1933
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: B94-002-1
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 VNEADGGR------YDCHLGGSLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-835-268-62
; Sequence 62, Application US/08835268
: Patent No. 5807826
; GENERAL INFORMATION:
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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677 K 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 -----NSAWLPVINSRVPEPRPGTCVNDT-----SNLPDTVINFIRSHPLMDKAVNHEHN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | : ::|| : ::|| | : ::|| | : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::|| : ::||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 HLVVDERIGHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTTN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 SVFGVIVS----YSNLDDXLFIATAV---DGKPEYFPTISSRKLTKNSEADGMFAYVFH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 DEFVASMIKIPSDTFTIIPDFDI-----YYVYGFSSGNFVYFLTLQP--EMVSPPGSTT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 KEQVYTSKLVRLCKEDTA-----FNSYVEVPIGCERSG---VEYRLLQAAYLSKAGA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 GKAVY-SRIARVCKKDVGGKNLLAHNWATYLKARLNCSISGEFPFYFNEIOSVY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
2.3%; Score 227; DB 1; Length 724;
Best Local Similarity 20.4%; Pred. No. 6.9e-11;
Matches 147; Conservative 118; Mismatches 260; Indels 196;
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Date Floppy disk
COPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: OSMAN, Richard A.
REGISTRATION NUMBER: 36.67
REGISTRATION NUMBER: 36.67
REGISTRATION NUMBER: 36.67
                         APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: Bentley, David R.
APPLICANT: Do'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESSED NONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                              STREET: SCIENCE & TECHNOLOGY LAW STREET: 268 Bush Street, Suite 3200 CITY: San Francisco STATE: CA COUNTRY: USA ZIONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415)343-4341
TELEFAX: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
Kolodkin, Alex L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-121-713D-62
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ua-09-964-956-13.raı

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
TLING DATE: US/09/060,692
FLING DATE: US/09/060,692
FLING DATE: 13-8F9-1993
ATFORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATFORNEY/AGENT INFORMATION:
NAME: Coman, Nichard & 6,627
REGISTRATION NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEKX: (415) 343-4441

09 53 09 72 09 113 09 120 09 1120 09 168 09 168 09 222
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| INFORMATION FOR SEQ ID NO: 62 | SEQUENCE CHRACATERISTICS: | LENGTH: 724 amino acids | TYPE: amino acid | TYPE: amino acid | MOLECULE TYPE: protein US-09-060-692-62

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168 SVFGVIVS----YSNLDDXLFIATAV---DGKPEYFPTISSRKLTKNSEADGMFAYVFH 219
                                                                                                                                                                                                                                                                            225 TDLYNTSAKRLEYKFYRTLKYDSKWLDKPNFVGSFDIGEYVYFFFRETAVEYIN----C 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 VLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDESALCIFILKQI----NDRIKERLQSCYR 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 ----NSAWLPVINSRVPEPRPGTCVNDT----SNLPDTVINFIRSHPLMDKAVNHEHN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 -----VFTE---DRDRMTSVIAYVYKNHSLAFVGTKSGKLKKIRVDGPRGNAL-QY 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 NPVYYKRDLVFTKLVVDKIR----IDILNQEYIVYYVGTNLGRIYKIVQYYRNGESLSKL 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 ETVQVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVESCG-QYQSCGECLGSGDPHCGW 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 CVLHNTCTRKER------CERSKEPRRFASEMKQCVRLTVHPNNISVSQYNVL 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 DKEANTCRPYELDLLQDVANETSDICDSSVLKKKIVVTYGQSVHLGCF------ 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 LVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQ 636
                                                                                                                                                                                                                                                                                                                                     220 DEFVASMIKIPSDTFTIIPDFDI-----YYVYGFSSGNFVYFLTLQP--EMVSPPGSTT 271
                                                                                 280 GKAVY-SRIARVCKKDVGGKNLLAHNWATYLKARLNCSISGEFPFYFNEIQSVY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 -----QLPSDKSRFFATFT----TSTNGLIGSAVCSFHINBIQAAFNGKFKEQSSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | :: | |: | |: | | | 486 LDIFEVAPNEAIQVMEISQTRKSLYIGTDHRIKQIDLAMCNRRYDNCFRCV--RDPYCGW
                                                                                                                                                                  113 NVNKMLLIDYKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKKEHY-----LSGVNESG
                                                                                                                                                                                                                                                                                                                                                                                                                      272 KEQVYTSKLVRLCKEDTA-----FNSYVEVPIGCERSG---VEYRLLQAAYLSKAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       377 GEGTLDLAWLKVKD--IPCSSALLTIDDNFCGLDMNAPLGVSDMVRGIP-----
Query Match 2.3%; Score 227; DB 2; Length 724;
Best Local Similarity 20.4%; Pred. No. 6.9e-11;
Matches 147; Conservative 118; Mismatches 260; Indels 196; Gaps
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ZIP: 94104 COMPUTER READABLE FORM:

336	169	949
592VKIPEVLKNEQVTWYHHSKDKGRYEIR-YSPTKYIETTERGLVVVS 636	637 LKSKEIGMIFASISFVFYNCSVHNSCLSCVESPYRCHWCKYRHVCTHDPKICSFQ 691	637 VNEADGGRYDCHLGGSLLCSYNITVDAHRCTPPNKSNDYQ 676
QQ	ò	qq

Db 637 VNEADGGR-----Qy 692 E 692
Db 677 K 677

Search completed: May 25, 2004, 04:26:25 Job time : 44 secs

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May 25, 2004, 03:50:55 ; Search time 82 Seconds (without alignments) 6449.214 Million cell updates/sec
                                                                                                                                                                                        US-09-964-956-13
9990
1 MKAMPWINTLLISHLLMVGM......QKLAYKLEQVITLMSLDSNK 1896
                                                                                                                                                                                                                                                                                                                                                                  1149313
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                         1149313 segs, 278921704 residues
                                                                         using sw model
                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                         OM protein - protein search,
                                                                                                                                                                                        Title:
Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Dat

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 13, Appl Sequence 9, Appli	43,	Sequence 44, Appl	Sequence 34, Appl	Sequence 81, Appl	Sequence 81, Appl	Sequence 32, Appl	Sequence 32, Appl	Sequence 42, Appl	Sequence 84, Appl	Sequence 84, Appl	Sequence 82, Appl	Sequence 82, Appl	Sequence 45, Appl
SUMMARIES	US-09-964-956-13 US-10-451-010-9	US-09-964-956-43	US-09-964-956-44	US-10-312-352-34	US-10-087-684-81	US-10-218-779-81	US-10-087-684-32	US-10-218-779-32	US-09-964-956-42	US-10-087-684-84	US-10-218-779-84	US-10-087-684-82	US-10-218-779-82	US-09-964-956-45
DB	12	13	13	12	12	12	12	12	12	12	13	12	12	12
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% Query Match	0.001	67.9	64.0	63.6	63.4	63.4	62.7	62.7	0.09	59.9	59.9	58.5	58.5	33.9
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US-09-964-956-4	US-10-276-774-2	US-10-276-774-207	US-10-0	US-10-108-260A-32	US-10-369-493-	US-10-276-774-212	-09-909-320-17	-09-909-088B-1	39-905-291A-	9-902-853-17	٣	9-907-841-17	US-09-904-011-1	US-09-906-74	0 US-09-906-838-170	US-09-907-613-	US-09-907-942-	US-09-904-859-1	US-09-909-204-17	US-09-904-820-17	US-09-904-786-1	US-09-906-646	US-09-906-100-17	US-09-903-78	US-09-902-903-	US-09-903-7	US-09-904-119-	US-09-904-956-17	
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ALIGNMENTS

RESULT 1 US-09-964-956-13

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Sequence 13, Application US/09964956 Publication No. US20040043326A1 GENERAL INFORMATION: APPLICANT: Gerlach, Valerie L APPLICANT: MacDougall, John R APPLICANT: Smithson, Glennda APPLICANT: Millet, Isabelle APPLICANT: Scone, David	APPLICANT: Gunther, Erik APPLICANT: Bllerman, Karen APPLICANT: Grosse, William M APPLICANT: Alsobrook II, John P APPLICANT: Lepley, Denise M APPLICANT: Burgess, Catherine E APPLICANT: Padigaru, Muralidhara APPLICANT: Kekuda, Ramesh APPLICANT: Kekuda, Ramesh APPLICANT: Leach, Martin D APPLICANT: Shinkets, Richard A APPLICANT: Shinkets, Richard A	Variable de la companie de la compan
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| Bublication No. US20040082761A1
| GENERAL INFORMATION:
| APPLICANT: INCYTE GENOMICS, INC.
| APPLICANT: DUGGAN, Brendan M. APPLICANT: LEE, Sally
| APPLICANT: US, Henry
| APPLICANT: WARREN, Bridget A. APPLICANT: WARREN, Bridget A. APPLICANT: GUGTER, Neil
| APPLICANT: GUGTER, Neil
| APPLICANT: BURPORD, Neil
| APPLICANT: BANDHAN, Olga
| APPLICANT: GALLICK, Deborah A. APPLICANT: GANDHI, Amena R. APPLICANT: GRAUL, Richard C. APPLICANT: GRAUL, Richard C. APPLICANT: GRAUL, Richard C. APPLICANT: GRAUL, Richard C. APPLICANT: GRAUL, Narinder K. APPLICANT: GRAUL, Narinder K. APPLICANT: LU, Yan
| APPLICANT: LU, Yan APPLICANT: LAL, Preefig.
| APPLICANT: LAL, Preefig. CURRENT FILMS DATE: 2003-06-17
| TITLE REFERENCE: PF-0667 USN CURRENT FILMS DATE: 2001-12-18
| PRIOR FILMS DATE: 2000-12-18
| PRIOR FILMS DATE: 2000-10-10-05
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99.9%; Score 9979; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1894; Conservative 0; Mismatches
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; OTHER INFORMATION: Incyte ID No: 7156379CD1
US-10-451-010-9
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ICATION NUMBER: 60/235,63 NG DATE: 2000-09-27 ICATION NUMBER: 60/235,63 NG DATE: 2000-09-27 ICATION NUMBER: 60/235,80 ICATION NUMBER: 60/235,00 ICATION NUMBER: 60/236,06	ICATION NUMBER: 60/236, MG DATE: 2000-09-27 ICATION NUMBER: 60/236, MG DATE: 2000-09-27 ICATION NUMBER: 60/236, MG DATE: 2000-09-28	LCATION NOMBER: 60/23/, 4 NG DATE: 2000-10-03 LCATION NUMBER: 60/238, 3 NG DATE: 2000-10-05 LCATION NUMBER: 60/238, 3 LCATION NUMBER: 60/238, 3 LCATION NUMBER: 60/238, 3 NG DATE: 2000-10-06 LCATION NUMBER: 60/238, 3 NG DATE: 2000-10-06	CATION 1 G DATE: CATION 1 G DATE: CATION 1 G DATE: EQ ID M	; SEQ ID NO 43 ; TYPE: PRT ; TYPE: PRT ; ORGANISM: Home sapiens 778-09-064-956-43	걸음적	PLSOKORSFVTFRG : PLSMEQRRPWPRALEVDSRSVVLLSVVWVLLAPPAAGMPQFSTFHS	Qy 50 GFNHLVVDERTGHIYLGANNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVOTCNEELT 109		Db 238 YGVIVRSEGEDGKLFIGTAVDGKQDYFPTLSSRKLPRDFESSAMLDYELHSDFVSSLIKI 297 Qy 230 PSDTFIIPDFDIYYVXGFSSGNFVYFLTLQPEMVSPPGSTTKEQVYTSKLVRLCKE 286	Db 298 PSDTLALVSHFDIFYIYGFASGGFVYFLTVQPETPEGVAINSAGDLFYTSRIVRLCKD 355 Qy 287 DTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGGKRK 346	Qy 347 MKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIPCSSALLTIDDNFCG 406	QY 407 LDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYYXRHSLAFVGTKSGKLKKIRVDGPRGN 466	40/ ALGIELVQVV-DFGFVLKBOKDRELLINGSBRKLINVFVBVBGLIGGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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Best Local Similarity 63.7%; Pred. No. 0;
Matches 1222; Conservative 245; Mismatches
PRIOR FILING DATE: 2001-05-31
PRIOR PELING DATE: 2001-05-31
PRIOR PELING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 44
LENGTH: 1905
TYPE: RRT
TYPE: RRT
CRGANISM: Xenopus laevis
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Sequence 34, Application US/10312322
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HENCORD, Nell; YAO, Monique G.
APPLICANT:
HENCORD, Nell; YAO, Monique G.
APPLICANT:
APPLICANT:
HENCORD, Nell; YAO, Monique G.
APPLICANT:
APPLICANT:
HENCORD, Nell; YAO, Monique G.
APPLICANT:
APPLICANT:
HENCORD, MAITAN R.
APPLICANT:
HENCORD, Nell; YAO, Monique G.
APPLICANT:
APPLICANT:
HO DAME A.
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Best Local Similarity 64.0%; Pred. No. 0;
Matches 1213; Conservative 258; Mismatches 401;
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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20040053824A1
US-10-312-352-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                       RDRGNVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTN
                                                     LLATKGTLOKFVDDLFETIFSTAHRGSALPLAIKYMFDFLDEQADKHGIHDPHVRHTWKS
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APPLICANT: MacDougal, John R.
APPLICANT: Miller, Isabelle
APPLICANT: Miller, Isabelle
APPLICANT: Biller, Isabelle
APPLICANT: Blosse, William M.
APPLICANT: Lepley, Denise M.
APPLICANT: Caren, David J.
APPLICANT: Caren, Davie M.
APPLICANT: Spycek, Kimberly A.
APPLICANT: Spycek, Kimberly A.
APPLICANT: Boldog, Perenc L.
APPLICANT: Boldog, Perenc L.
APPLICANT: Boldog, Perenc L.
APPLICANT: Miller, Vishuu
APPLICANT: Miller, Vishuu
APPLICANT: Malara Vishuu
APPLICANT: Shenoy, Suresh G.
APPLICANT: Rastelli, Luca
APPLICANT: Carines A.M.
APPLICANT: Carines A.M.
APPLICANT: Carines A.M.
APPLICANT: Carines M. Since M.
APPLICANT: Carines M. Staojia
APPLICANT: Gargolli, Esha A.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-214 C.P.
CURRENT APPLICANT: MALBER: US/10/087,684
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US-10-087-684-81
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PRIOR APPLICATION NUMBER: 60/253,834
PRIOR FILING DATE: 2000-11-29
PRIOR PELLING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR APPLICATION NUMBER: 60/264,180
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR FILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 220
SOFTWARE: CuraSeqList version 0.1
1 PANCTH. 1894

; TYPE: PRT ; ORGANISM: Mus musculus US-10-087-684-81

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                                                                                                                          59 GEVYVGAVNRIYKLSGNITILRAHVTGPVEDNEKCYPPPSVQSCPHGLGSTDNVNKLILL
                                                                                                                                                                                                                     LDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIP
                                                                                                                                                                                                                                     GQAKLFVGTPIDGKSEYFPILSSRRLMANBEDADMFGFVYQDEFVSSQLKIPSDTLSKFP
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                                                                       GHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCYPPRIVQTCNEPLTTINNVNKMLLI
                                                      1 MKAMPWNWTCLLSHLLMVGMGSSTLLTRQPAPLSQKQRSFVTFRGEPAEGFNHLVVDERT
                             Gaps
                           20;
  Length 1894;
                             Indels
Query Match 63.4%; Score 6337; DB 12; Best Local Similarity 63.5%; Pred. No. 0; Matches 1209; Conservative 267; Mismatches 408;
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                                                                                                                                                                                                                                                                           1017 HTPGSAPIVININRAQLSNPEVKYNYTEDPTILRIDPEWSINSGGTLLTVTGTNLATVRE 1076
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                                                                                                                                                                  897 GVHVGKVLCSPVESEYISAEQIVCEIGDASTLRAHDALVEVCVRDCSLHYRALSPKRFTF 956
                                                                                                             1432 ESVAEKALINWFTFLLYKFLKECAGEPLFMLYCAIKQQMEKGPIDAITGEARYSLSEDKL
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                                                        834 LROHCPAGE-SOWLELSGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIAS
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1196	OY 1256 LVI	Qy 1311 GIE 	Qy 1371 TLE Db 1372 TLE	1431	Oy 1491 IR(Db 1492 IR(1551	Oy 1611 ST	1671	1731	1791	DD 1851 HE	RESULT 8 US-10-087-684-32 ; Sequence 32, A) ; Publication No	; APPLICANT: BG; APPLICANT: BG; ; APPLICANT: M:				APPLICANT: M APPLICANT: S APPLICANT: R APPLICANT: T APPLICANT: T	, APPLICANT: Z
121 DYKENRLIACGSLYQGICKLIRLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSN 178 	179 LDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMFAYVFHDEFVASMIKIPSDTFTIIP 238	239 DFDIYYVYGFSGNFVYFLTLQPBMVSPPGSTTKBQVYTSKLVRLCKEDTAFNSYVEV 296 239 AFDIYYVYSFRSBOFVYYLTLGLDYGLTSPDAAGEHFFYSKLVRLCVMDPKFYSYVEF 296	PIGCERSCUEYRLLQAAYLSKAGAVLGRTLGVHPDDDLLFTVFSKGQKRKMKSLDBSALC	FIGURE GARGE FIGURE FIGU	417 DMVRGIPVFTEDRDRMTSVIAVVYRMHSLAFVGTKSCKLKKIRVDGPRGN-ALQYETV 473 :	QVVDPGPVLRDMAFSXDHEQLYIMSERQLTRVPVESCGQYQSCGECLGSGDPHCGWCVLH	534 NTCTRKERCERSKEPRREASEMKQCVRLTVHPNNISVSQYNVLVLVLETYNVPELSAGVNC 593 5	TPEDLSEMDGLVVGNQIQCYSPAAKEVPRIITENGDHHVVQLQLKSKETGMTFASTSFVF			774 INNLPVELTVVWNGHFNIDNPAQNKVHLYKGGAMRESCGLCLKADPDFACGWCQGPGQCT 833 ::	00 00 0	HVKVAGGECSELVIDGILFAEQILCEMGEAKESQTAGGEVEICVAVCKEEFFFAKSSQLIII 	952 MTLTLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVCNTTSS 1011 :	1012 DEVLEMKVSVQVDRAKI-HQDLVFQYVEDFTIVRIEPEWSIVSGNTPIAVWGTHLDLIQN 1070 	1071 PQIRAKHGGKEHINICEVLANATEMTCQAPALALGPDHQSDLTERPEEFGFILDNVQSLLI 1130 :	1131 LNKINFTYYPNPVFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPC 1190 	1191 TVTVSDVQLLCESPNLIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLI 1250
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Bdinger, Shlomit R.
Bdinger, Shlomit R.
MalDedjall, John R.
Millet, Isabelle
Ellerman, Karen
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Ellerman, Karen
Stone, David J.
Grosse, William M.
Iepley, Denise M.
Reger, Daniel K.
Burgess, Cathereine E.
Casman, Stacie, J.
Ellerman, Stacie, J.
Ellerman, Muralidhara
Mishra, Vishnu
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327 YRLVQDAYLSRPGRALAHQLGLAEDEDVLFTVFAQGGONRVKPPKESALCLFTLRAIKEK 386
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APPLICANT: Malyankar, Uriel M.
APPLICANT: Guo, Xiaojia
APPLICANT: Guo, Xiaojia
APPLICANT: Miler, Charles E.
APPLICANT: Gangolli, Esha A.
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TILLS PRERERNES: 21402-214 CIP
CURRENT FILING DATE: 2003-03-10
FRIOR APPLICATION NUMBER: 60/253,834
FRIOR APPLICATION NUMBER: 60/256,926
FRIOR APPLICATION NUMBER: 60/264,180
FRIOR APPLICATION NUMBER: 60/264,180
FRIOR APPLICATION NUMBER: 60/274,194
FRIOR APPLICATION NUMBER: 60/274,194
FRIOR APPLICATION NUMBER: 60/313,656
FRIOR APPLICATION NUMBER: 60/313,656
FRIOR APPLICATION NUMBER: 60/313,656
FRIOR APPLICATION NUMBER: 60/327,456
FRIOR APPLICATION NUMBER: 60/3213,656
FRIOR APPLICATION NUM
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APPLICANT: Kekuda, Rameeh
APPLICANT: Spycker, Kimberly A
APPLICANT: Shinkers, Michael A
ITILE REFERENCE: 21402-124
CURRENT FILMS OF INVENTIONS: US/09/964,956
CURRENT FILMS OF MATE: 2001-09-27
FRICA PAPLICATION NUMBER: 60/235,631
FRICA FILMS OF STREET 2000-09-27
FRICA FILMS OF STREET 2000-00-27
FRICA FILMS OF STREET 2000-00-67
FRICA FILMS OF STREET 2000-10-06
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                                                                                                           SDVQLLCESPNLIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLIIFIV
                                                                                                                                                                                                    AVLIAYKRKSRDADRTLKRLQLQMDNLESRVALECKEAFAELQTDIHELTNDLDGAGIPF
                                                                                                                                                                                                                                                                                                                                                            LDYRTYTMRVLFPGIEDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIRTLES
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                                                                              1135 NFTYYPNPVFEAFGPSGILELKPGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVTV
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US-09-964-956-956
Publication No. US20040043926A1
GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: Santhson, Glenda
APPLICANT: Stone, David
APPLICANT: Stone, David
APPLICANT: Glenda
APPLICANT: Glenda
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APPLICANT: Glenda
APPLICANT: Alsobrook II, John P
APPLICANT: Alsobrook II, John P
APPLICANT: Buepley, Denise M
APPLICANT: Buepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara

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189
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SASFVYFLTLQLDTQQTLLDTAGEKFFTSKIVRMCAGGSEFYSYVEFPIGCSWRGVEYRL
                                                                                                                           CLLL-LLFLAVGGA--LGNRPF-----RAFVV----TDTTLTHLAVHRVTGBVFVGAVN
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                                                                                  Gaps
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                                                       DB 12; Length 1871;
                                                    Query Match
Best Local Similarity 60.0%; Pred. No. 0;
Matches 1133; Conservative 295; Mismatches 435; Indels
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-956-42
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LGGLHVIEGLPLLA	VQVVDPGPVLRDMAI : : VPVVDGSPILRDLL	HNTCTRKERCERSKU : : RHRCCREGACLGAS/	ASEMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDG-LVVGN 	VFYNCSVHNSCLSC VFYNCSVLQSCMSC	VPVEVIKPITLKAKI PVGVMQPLTLRAKI	MEINNLPVELTVVW : : : DEHGDTELDFSVVWI	CTLROHCPAQESOW) : COLRTHCPAPKTNW	SHVKVAGVECSPLVI :: :: LRVAGVRCNSIPA	PAEQIVCEMGEA-KPSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGFMS : : :	QVTITGTNLNAGSNVVVMFGKQPCLFHRRSPSYIVC-NTISSDBVLEMKVSVQVDRA 	ONPOIRAKHGGKEH: :: : OEPRVRAKYRGIET"	EVINATEMTCQAPALALGFDHQSDLTERPEEFGFILDNVQSLLIINKTNFTYYPNPVFE -	PSGILELKRGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVTVSDVQLLCESPN 	LIIFIVAVLIAYKR :: : LLLAITAVLVAYKR	RLQWQWDNLESRVALECKEAFAELQTDIHELTSDLDGAGIPFLDYRTYTMRVL :	PGIEDHPVLRDLEVPGYRGERVEKGLKLFAQLINNKVFLLSFIRTLESGRSFSMEDRGN PGIEAHPVLKELDTPPNVEKALRLFGQLLHSRAFVLTFIHTLEAQSSFSMRDRGT	RTESVAEKMLTNWF RTESVAEKMLTNWF	KLIRQQIDYKTLVL
: : QINGNFCGLVLNQP	RVDGPRGNALQYET : : RVDGFQ-DAHLYET	CLGSGDPHCGWCVL.	LETYNVPELSAGVN: :: : vTLHNVPDLSAGVS	QCYSPAAKEVPRIITENGDHHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCLS : :	PEDCPQLLRVDKIL : PEGCPEILPSGDLL	SSVQCQNTSYSYEG	DPDFACGWCQGPGQ DPRFNCGWCISEHR	IRGENLGLEFRDIA : VGDNLGLLSREVG	CRPEFMARSSOLYY : : : CSADFRTQSEQVYS	HRRSPSYIVC-NTT : VRRDAKAIVCISPL	NTPIAVWGTHLDLI - - -	PEEFGFILDNVQSL : : : PDEFGFLLDHVQTA	GNVKLNYTVLVGEK : : : : :SS-RLNYTVLIGGQ	SLPAIVSIAVAGGL 	relotdiheltsder :: Slotdineltheme	EDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIRTLESQRS :: :	OKNLESKNHPKLLLE KNLESKNHPKLLLE	IDAITGEARYSLSEI
:: :: #LLNKELPCINTPM	LAFVGTKSGKLKKI : : : : VVFIGTRSGSLKKV	VPVESCGQYQSCGE : : LPVETCEQYQSCAA	PNNISVSQYNVLLV : : NNSVTSPGVQLT	ITENGDHHVVQLQL : - RGHGATRTVRLQL	DPKTCSFQEGRVKL 	QGSEQRVPALRFNS : QGRQQRVPAVRFNS	CGAMRESCGLCLKA 	IPVTGPREGGTKVT : : HPLVGPKEGGTRVT	PSQHAGFVEICVAV SPPPGPVELCVGD	SNVVVMFGKQPCLF 	TIVRIEPEMSIVSG : : TVTRLEPTWSIING	LALGPDHQSDLTER : IFLGRPQPRAQGEH	IILKGKNLIPPVAG :: vvLKGKNLIPAAAG	YSPGMVYIAPDSPL : :: : FWLGTLHISAERAL	LESRVALECKEAFA LESRVALECKEAFA	PGYRQERVEKGLKI 	ATDVLKQLLADLII : ATGLLKQLLADLIE	:
:	DRMISVIAYVYROHSLAFVGIKSGKLKKIRVDGFRGNALQYETVQVVDPGFVLRDMAFS: 	DHEQLYIMSERQLIRVPVESCGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPR : :: : :	REASEMKQCVRLTVHPNNISVSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDG-LVVGN 	QIQCXSPAAKEVPRIITENGDHHVVQLQLKSKETGMTFASTSFVFXNCSVHNSCLSCVES ::	PYRCHWCKYRHVCTHDPKTCSFQBGRVKLPEDCPQLLRVDKILVPVBVIKPITLKAKNLP 	QPOSGQRGYECILNIQGSEQRVBALRENSSSVQCQNTSYSYEGMEINNLPVELTVWMNGH 	FNI DNPAQNKVHLYKCGAMRESCGLCLKADPDFACGWCGGPGCTLRQHCPAQESQMLEL 	SGAKSKCTNPRITEIIPVTGPREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGY :: : : : :	PAEQIVCEMGEA-K : : SAERIVCEMEESLV	5-5	KIHQ-DLVFQYVEDPTIVRIEPEMSIVSGNTPIAVMGTHLDLIQNPQIRAKHGGKEHINI 	CBVINATBMTCQAPALALGPDHQSDLTERPEEFGFILDNVQSLLILNKTNFTYYPNBVFF - - - - -	AFGPSGILBLKRGTPIILKGKNLIPPVAGGNVKLNYTVLVGEKPCTVTVSDVQLLCESPN	LIGRHKVWARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYRRKSR 	esdlilkelomondlesrvaleckeafaelotdiheltsdlogagipfloyrtytmrul ::	FPGIEDHPVLRDLEV : : FPGIEAHPVLKELDI	VASLIMTVLOSKLEYATDVLKOLLADLIDKNLESKNHPKLILRRTESVAEKMLTNWFTFL 	LYKFLKECAGEPLFSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLS -
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                               IPAEQIVCEMGEA-KPSQHAGFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMS
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FPIDKPPSFRALLYKCWAQRPSCGLCLKADPRFNCGWCISEHRCQLRTHCPAPKTNWMHL
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Best Local Similarity 60.0%; Pred. No. 0;
Matches 1133; Conservative 293; Mismatches 437;
                                                                                  ) ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

: LOCATION: (380)..(380)

; OTHER INFORMATION: Wherein Kaa may be any

US-10-087-684-84
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION WUMBER: 60/327,456
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 220
SOFTWARE: CaraSequist version 0.1
SEQ ID NO 84
                                                                       TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .30 CGSLYQGICKLLRLEDLFKLGEPYHKKEHYLSGVNESGSVFGVIVSYSNLDDKLFIATAV 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fatcutajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Tastelli, Luca
APPLICANT: Corine
APPLICANT: Cerhusen, Eryan
APPLICANT: Zerhusen, Bryan
APPLICANT: Zerhusen, Bryan
APPLICANT: Maller, Charles
APPLICANT: Miller, Charles
APPLICANT: ON NUMBER: 00/253,834
FRIOR APPLICATION NUMBER: 60/253,834
FRIOR APPLICATION NUMBER: 60/250,-926
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2001-11-30
FRIOR FILING DATE: 2001-10-05
FRIOR FILING DATE: 2001-00-25
FRIOR APPLICATION NUMBER: 60/313,656
FRIOR APPLICATION NUMBER: 60/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
59.9%; Score 5988; DB 12; Length 1871;
Best Local Similarity 60.0%; Pred. No. 0;
Matches 1133; 'Conservative 293; Mismatches 437; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (380)
CTHER INFORMATION: Wherein Xaa is any amino acid.
US-10-218-779-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li, Li,
Padigaru, Muralidhara
Mishra, Viehnu
Patturajan, Meera
Shenoy, Suresh
                                                                                          Sequence 84, Application US/10218779
Publication No. US20040029222A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                Elleman, Karen
Stone, David
Gerlach, Valerie
Grosse, William
Alsobrook II, John
Lepley, Denise
Kieger, Daniel
Burgess, Catherine
Casman, Stacie
Spytek, Kimberly
Boldey, Ferenc
                                                                                                                                                            APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John
APPLICANT: Milet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGAL:...

TYPE: PT
ORGANIEM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
'^^*TION: (380)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1806 SYKNWVERYYSDIGKMPAISDQDMNAYLAEQSRMHMNEFNTMSALSEIFSYVGKYSEEIL 1865
                                                                                                                                                                           1364 VASLTMVALQSRLDYATGLLKQLLADLIEKNLESKNHPKLLLRRTESVAEKMLTMWFTFL 1423
                                                                                                                                                                                                                                 1446 LYKFLKECAGEPLFSLFCAIKOOMEKGPIDAITGEARYSLSEDKLIROQIDYKTLVLSCV 1505
                                                                                                                                                                                                                                                        1626 RYTGSPDSLRSRTPMITPDLESGVROWHLVRONHEHGDQKEGDRGSKOVSEIYLTRLLATK 1685
                        1544 QDEDVITKIECDWKRLNSLAHYQVIDGSLVALVPKQVSAYNMANSFIFTR-SLSRYESLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESDLTLKRLQMQMDNLESRVALECKEAFAELQTDIHELTSDLDGAGIPFLDYRTYTMRVL
                                                                                                                                                                                                                                                                                                                                                                                       ODEDITIKI BNDWKRINTLAHYQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYENMI
                                                                                                                                                       1386 VASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1746 RFWVNMIKNPQFVFDIHKNSITDACLSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1866 GPLDHDDQCGKQKLAYKLEQVITLMSLDS 1894
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US-10-087-684-82
Sequence 82, Application US/10087684
Publication No. US2004002916A1
GENERAL INFORMATION:
APPLICANT Edinger, Shlomit R.
APPLICANT Edinger, Shlomit R.
APPLICANT Ellerman, Karen
APPLICANT Ellerman, Karen
APPLICANT Gross, William M.
APPLICANT Ellerman, Karen
APPLICANT Stone, David J.
APPLICANT Stone, David J.
APPLICANT Stone, David J.
APPLICANT Rieger, Daniel K.
APPLICANT BUTGES, Cathereine E.
APPLICANT BOLOGY, Ferenc L.
APPLICANT BOLOGY, Ferenc L.
APPLICANT Radigaru, Muralidhara
APPLICANT Radigaru, Muralidhara
APPLICANT Radigaru, Wishnu
APPLICANT Ratelli, Luca
APPLICANT Ratelli, Luca
APPLICANT Schook, Suresh G.
APPLICANT Corine A.M.
APPLICANT Corine A.M.
APPLICANT Cernusen, Siyan D.
APPLICANT Cernusen, Bryan D.

*** FEATURE: DCATION: (78) ... (74) ... (7474) ... (7474) ... (7474) ... (7474) ... (7474) ... (7474) ... (7474) ... (7474) ... (7474) ... (7474) ... (7876.84-82 273 EQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDD 332
253 EHFFTSKIVRLCVDDPKFYSYVEFPIGCEQAGVEYRLVQDAYLSRPGRALAHQLGLAEDE 312 CSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVLAVVKNHSLAFVGTKS 452 215 AYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQ--PEMVSPPGSTTK 272 DLLFTVFSKGOKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIP 392 16 QPPFRTFSGSD-WGLTHILVHEQTGEVYVGAVNRIYKLSGNLTILRAHVTGPVEDNEKCX 97 PPRIVQTCNEPLITINNVNKWLLIDYKENRLIACGSLYQGICKLLRLEDLFKLGEPYHKK 37 QRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCY Query Match 58.5%; Score 5847.5; DB 12; Length 1754; Best Local Similarity 63.7%; Pred. No. 0; Matches 1114; Conservative 237; Mismatches 378; Indels 19; Gaps APPLICANT: Guo, Xiaojia
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
TITLE OF INVENTION: BEABA A.
TITLE OF INVENTION: BEOTHERS AND NUCLBIC ACIDS ENCODING SAME FILE REFERENCE: 214 C.P
CURRENT APPLICATION NUMBER: US/10/087,684
CURRENT FILING DATE: 2000-11-29
PRIOR PELING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR APPLICATION NUMBER: 60/24,180
PRIOR APPLICATION NUMBER: 60/24,180
PRIOR PELING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/274,194
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-03-06
PRIOR FI 333 393

973 SVGGRPCSFSWRNSREIRCLTPPGQSPGSAPIIININRAQLTNPEVKYNYTEDFIILRID 1032 1107 HQSDLTERPEEFGFILDNVQSLLILNKTNFTYYPNPVFEAFGPSGILELKPGTPIILKGK 1166 1227 YIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSRESDLILKRLOMOMDNLESRVA 1286 RVEKGLKLFAQLINNKVFLLSFIRTLESQRSFSWRDRGNVASLIMTVLQSKLEYATDVLK 1406 MFGKQPCLFHRRSPSYIVCNTTSSDEVLEMKVSVQVDRAKI-HQDLVFQYVEDPTIVRIE 1046 1033 PEWSINSGGILLTVIGINLATVREPRIRAKYGGIERENGCLVYNDTIMVCRAPSVANPVR 1092 LECKEAFAELQTDIHELTSDLDGAGIPFLDYRTYTMRVLFPGIEDHPVLRDLEVPGYRQE 1346 OLLADLIDKNLESKNHPKLLLRRTESVABKMLTNWFTFLLYKFLKECAGEPLFSLFCAIK 1466 QOMEKGPIDAITGEARYSISEDKLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDTIT 1526 PEWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTCQAPALALGPD 1106 NLIPPVAGGNVKLNYTVLVGEKPCTVTVSDVQLLCESPNLIGRHKVMARVGGMEYSPGMV 1226 FORGRVKLPEDCPQLLRVDXILVPVEVIKPITLKARNLPOPQSGGRGYECILNIQSSEQR 749 VTALRENSSSLQCQNSSYSYEGNDVSDLPVALSVVWNGNFVIDNPQNIQAHLYKCPALRE 792 ALVEVCVRDCSPHYRALSPKRFTFVTPTFYRVSPSRGPLSGGTWIGIEGSHLNAGSDVAV 972 SCGLCLKADPDFACGWCQGPGQCTLRQHCPAQ-ESQWLELSGAKSKCTNPRITEIIPVTG 868 PREGGIKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEMGEAKPSQ-HA 927 CGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRFASEMKQCVRLTVHPNNIS SCGLCLKADPRFECGWCVAERRCSLRHHCAADTPASWMARHGSSRCTDPKILKLSPETG HHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYRHVCTHDPKTCS VPALRENSSSVQCQNTSYSYBGMEINNLPVELTVVWNGHENIDNPAQNKVHLYKCGAMRE QOMEKGPIDAITGEARYSLSEDKLIRXQIDYKTLTINCVNPENENAPEVPVKGLDCDTVT CINSPLQIDDDFRGQDFNQPLGGTVTIEGTPLFVDKDDGLTAVAAYDYRGRTVVFAGTRS VSQYNVLLVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRITTENGD GFVEICVAVCRPEFMARSSQLYYFMTLTLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVV GKLKKIRVD--GPRGN-ALQYETVOVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVES 1272 1407 373 493 570 553 630 613 673 733 913 988 1047 1167 1153 1287 1347 1388 1467 1448 453 510 690 750 810 793 869 853 928 8 8 8 ò 임 δ g $\dot{\circ}$ Ob ò qq ò

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YQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYENMIRYTGSPDSLRSRTPMITPDLE SGVKMMHLVKNHEHGDQKEGDRGSKMVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRG

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1687 SALPLAIKYMFDFLDEQADKHQIHDADVRHTWKSNCLPLRFWVNVIKNPQFVFDIHKNSI 1746

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SALPLAIKYMFDFLDEQADKHGIHDPHVRHTWKSNCLPLRFWVNMIKNPQFVFDIHKNSI

1627 SGTKLWHLVKONHDHLDQREGDRGSKONVSEIYLTRLLATKGTLQKFVDDLFETIFSTAAHRG

APPLICANT: MacDougall, John
APPLICANT: MacDougall, John
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David
APPLICANT: Stone, Valerie
APPLICANT: Gresse, William
APPLICANT: Gresse, William
APPLICANT: Alegiev, Danise
APPLICANT: Bejdey, Denise
APPLICANT: Bejdey, Denise
APPLICANT: Bejdey, Milliam
APPLICANT: Bejdey, Milliam
APPLICANT: Bejdey, Kimberly
APPLICANT: Bejdey, Kimberly
APPLICANT: Beldey, Kimberly
APPLICANT: Beldey, Kimberly
APPLICANT: Beldey, Welizar
APPLICANT: Benev, Vishau
APPLICANT: Branelli, Luca
APPLICANT: Beldey, Grise
APPLICANT: Beldey, Wilsar
APPLICANT: Gangolli, Esha
APPLICANT: Miler, Carales
APPLICANT: Miler, Carales
APPLICANT: Miler, Carales
APPLICANT: Miler, Carales
APPLICANT: Miler, Larles
APPLICANT: Miler, Carales
APPL Sequence 82, Application US/10218779; Sequence 82, Application US/10218779; Publication No. US20040029222A1
GENERAL INFORMATION: Shlomit
APPLICANT: Edinger, Shlomit
APPLICANT: Mallet, Isabelle
APPLICANT: Blerman, Karen
APPLICANT: Grone, David
APPLICANT: Grose, William
APPLICANT: Grose, William
APPLICANT: Lepley, Denise
APPLICANT: Rieger, Daniel
APPLICANT: Rieger, Daniel
APPLICANT: Seger, Daniel
APPLICANT: Syvek, Kimberly
APPLICANT: Syvek, Kimberly
APPLICANT: Soldog, Ferenc

RESULT 15 US-09-964-956-45 1047 1033 1107 1093 1167 1227 793 853 928 913 973 1287 698 733 810 8 6 6 6 6 868686 ò - 유 g ઠે 유 ò ઠે 셤 8 8 g à g ò g જે d 8 8 8 ò 749 809 569 612 689 672 732 432 509 552 629 12, 156 134 272 332 392 452 194 96 74 CVQYTSCELCLGSRDPHCGWCVIHSICSRRDACERADEPQRFAADLLQCVQLTVQPRNVS HHVVQLQLKSKETGMTFASTSFVFYNCSVHNSCLSCVESPYRCHWCKYRHVCTHDPKTCS FLEGRVNVSEDCPQILPSTQIYVPVGVVKPITLAARNLPQPQSGQRGYECLFHIPGSPAR VPALRENSSSVQCQNTSYSYEGMEINNLPVELTVVWNGHFNIDNPAQNKVHLYKCGAMRE CGQYQSCGECLGSGDPHCGWCVLHNTCTRKERCERSKEPRRFASEMKQCVRLTVHPNNIS VSQYNV1LVLETYNVPELSAGVNCTFEDLSEMDGLVVGNQIQCYSPAAKEVPRITTENGD FOEGRVKLPEDCPOLLRVDKILVPVEVIKPITLKAKNI POPOSGORGYECILNI QGSEQR PPRIVQTONEPLITINNVNKMLLIDYKENRLIACGSLYQGICKLIRLEDLFKLGEPYHKK **EQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDD** DLL FTV FSKGOKRKMKSLDESALCI FILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIP CSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKS GKLKKIRVD--GPRGN-ALQYETVQVVDPGPVLRDMAFSKDHEQLYIMSERQLTRVPVES EHYLSGVNESGSVFGVIVS - - YSNLDDKLFIATAVDGKPEYFPTISSRKLTKNSEADGMF 215 AYVFHDEFVASMIKIPSDIFTIIPDFDIYYVYGFSSGNFVYFLTLO--PEMVSPPGSTTK QRSFVTFRGEPAEGFNHLVVDERTGHIYLGAVNRIYKLSSDLKVLVTHETGPDEDNPKCY Gaps Length 1754, 19; Query Match 58.5%; Score 5847.5; DB 12; Lengt Best Local Similarity 63.7%; Pred. No. 0; Matches 1114; Conservative 237; Mismatches 378; Indels acid. acid ; OTHER INFORMATION: Wherein Xaa is any amino acid US-10-218-779-82 amino amino amino any any : :-: 19 18 ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: VARIANT
LOCATION: (78)
OTHER INFORMATION: Wherein Xaa is
FEATURE:
NAME/KEY: VARIANT
LOCATION: (123)
OTHER INFORMATION: Wherein Xaa is
FEATURE:
NAME/KEY: VARIANT
LOCATION: (620)
OTHER INFORMATION: Wherein Xaa is
FEATURE:
NAME/KEY: VARIANT
LOCATION: (620)
OTHER INFORMATION: Wherein Xaa is
FEATURE:
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1474) 750 510 493 570 690 673 313 393 373 453 433 37 97 75 157 135 273 253 333 16 6 8 6 8 6 8 6 8 6 90 A2 A90 엄 8 8 8 δ Db à g

1466 1746 1406 1387 1447 1586 1106 1286 1271 988 MFCKQPCLFHRRSPSYIVCNTTSSDEVLEMKVSVQVDRAKI-HQDLVFQYVEDPTIVRIE 1046 972 987 852 927 QLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWPTFLLYKFLKECAGEPLFSLFCAIK QVKEKILDAIFKAVVPCSHRPKAADMDLEWRQGSGARMILQDEDITTKIENDWKRLNTLAH 1347 RVEKGLKLFAQLINNKVFLLSFIRTLESQRSFSMRDRGNVASLIMTVLQSKLEYATDVLK SGVKMWHLVKNHEHGDQKEGDRGSKMVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRG SGTKLWHLVKNHDHLDQREGDRGSKAVSEIYLTRLLATKGTLQKFVDDLFETIFSTAHRG YQVPDGSVVALVSKQVTAYNAVNNSTVSRTSASKYENMIRYTGSPDSLRSRTPMITPDLE PEWSIVSGNTPIAVWGTHLDLIQNPQIRAKHGGKEHINICEVLNATEMTCQAPALALGPD YIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKRKSRESDLTLKRLQMQMDNLESRVA LECKEAFAELQTDIHELTSDLDGAGIPFLDYRTYTMRVLFPGIEDHPVLRDLEVPGYRQE QQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLSCVSPDNANSPEVPVKILNCDTIT PREGGTKVTIRGENLGLEFRDIASHVKVAGVECSPLVDGYIPAEQIVCEMGEAKPSQ-HA NLIPPVAGGNVKLNYTVLVGEKPCTVTVSDVQLLCESPNLIGRHKVMARVGGMEYSPGMV GFVEICVAVCRPEFMARSSQLYY FWTLTLSDLKPSRGPMSGGTQVTITGTNLNAGSNVVV VTALR FNSSSLQCQNSSYSYEGNDVSDL PVNLSVVWNGNFVI DNPQNI QAHLYKCPALRE SCGLCLKADPDFACGWCQGPGQCTLRQHCPAQ-ESQWLELSGAKSKCTNPRITEIIPVTG TDACLSVV 1407 (1568 1467 1508 1647 1707 1687 1767 1527 1587 1627 1747

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                                                    GRAERAL WRORMANION, Walerie L
APPLICANT: GETACA, Walerie L
APPLICANT: GETACA, Walerie L
APPLICANT: Matthon, Genda
APPLICANT: SELDIE CONTRACTOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLIGRHKVMARVGGMEYSPGMVYIAPDSPLSLPAIVSIAVAGGLLIIFIVAVLIAYKKS 1264
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79.1%; Pred. No. 1.5e-299;
:ive 76; Mismatches 92;
Sequence 45, Application US/09964956
Publication No. US20040043926A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 79.14
Matches 641; Conservative
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; ORGANISM: Homo sapiens
US-09-964-956-45
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1805 PSYKNWYERYYSDIGKMPAISDQDMNAYLAEQSRAHMNEFNTMSALSEIFSYVGKYSEEI 1864
724 PSYKSWYERYYADIAKLPAISDQDMNAYLAEQSRLHAVEFNMLSALNEIYSYVSKYSEEL 783
                                                                                        1325 LFPGIEDHPVLRDLEVPGYRQERVEKGLKLFAQLINNKVFLLSFIRTLESQRSFSMRDRG 1384
                                                                                                                                                                                                                                    1385 NVASLIMTVLQSKLEYATDVLKQLLADLIDKNLESKNHPKLLLRRTESVAEKMLTNWFTF 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1505 VSPDNANSPEVPVKILNCDTITQVKEKILDAIFKNVPCSHRPKAADMDLEWRQGSGARMI 1564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1685 KGTLQKFVDDLFETIFSTAHRGSALPLAIKYMFDFLDEQADKHGIHDPHVRHTWKSNCLP 1744
                                                                                                                                                                                                                                                                            304 NVASLIMIGLOGRLEYATDVLKQLLSDLIDKNLENKNHPKLLLRRTESVAEKMLTNWPAF 363
                                                                                                                                                                                                                                                                                                                                                                                                         364 LIHKFLKECAGEPLFWLYCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIEXKTLILNC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 FRYTGSPDSLRSRAPMITPDLESGVKVWHLVKONHDHGDQKEGDRGSKMVSEIYLTRLLAT 603
1445 LLYKFLKECAGEPLFSLFCAIKQQMEKGPIDAITGEARYSLSEDKLIRQQIDYKTLVLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      604 KGTLQKFVDDLFETLLSTVHRGSALPLAIKYMFDFLDEQADRHSIHDTDVRHTWKSNCLP
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124 NLTGQHKVMVHVGGMVFSPGSVSVISDSLLTLPAIVSIAAGGSLLLIIVIIVLIAYKRKS 183

1265

Search completed: May 25, 2004, 04:27:57 Job time : 94 secs

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-DB=16sued_Patente NA -OFMT=fastap -SUFFIX=rni -MINMATGH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=1 -MARRIX=blosum62 -TRANS=human40 -cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPDIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRE=4059666956 @CGN 1 175 @runat 19052004 160715 10947 -NOPU=6 -ICPU=3
-NO MMAP -LARGEGUERY -NDG_SCORES=0 -MAIT -DSPBLOCK=700 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREAPDI=10 -XGAPEXT=0.5 -FGAPEPE6
-FGAPEXT=7 -YGAPEDP=10 -YGAPEXT=0.5 -DELEXT=7
                                                     May 23, 2004, 12:26:29 ; Search time 178 Seconds (without alignments) 5911.162 Million cell updates/sec
                                                                                      US-09-964-956-13
9990
1 MKRAMPWNWTCLLSHLLMVGM.....QKLAYKLEQVITLMSLDSNK 1896
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                        nucleic search, using frame_plus_p2n model
                                                                                                                                                                                        hits satisfying chosen parameters:
                                                                                                                                                                       682709 seqs, 277475446 residues
                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Perfect score:
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11, Appli 5, Appli 61, Appli 61, Appli 61, Appli 61, Appli 61, Appli 61, Appli 62, Appli 63, Appli 64, Appli 65, Appli 66, Appli 66, Appli 66, Appli 66, Appli 67, Appli 68, Appli 6

Sequence Seq

US-09-077-940A-1
US-09-653-274-3
US-09-653-274-3
US-08-835-274-3
US-08-835-274-3
US-08-835-268-61
US-08-833-391-61
US-09-653-274-12
US-08-833-391-53

ALIGNMENTS

APPLICANT: Genentech, Inc.
APPLICANT: Abthemat, Avi
APPLICANT: Battein, David
APPLICANT: Botstein, Dan L.
APPLICANT: Batton, Dan L.
APPLICANT: Fatron, Dan L.
APPLICANT: Fatron, Dan L.
APPLICANT: Fatron, Mary E.
APPLICANT: Forg, Sherman
APPLICANT: Gener, Hamspeter
APPLICANT: Gener, Hamspeter
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Mather, Jenses
APPLICANT: Mather, Jenses
APPLICANT: Roy, Margaret Ann
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Milliam, I.
TITLE OF INVENTION: Acidete and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acidete Encoding the Same
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/09/907,794A APPLICANT: 6635468

JENDERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Betherati, Avi
APPLICANT: Betherati, Avi
APPLICANT: Betherati, David
APPLICANT: Betherati, David
APPLICANT: Ferrara, Napoleone
APPLICANT: Franca, Napoleone
APPLICANT: Fong, Sherman
PPLICANT: Fong, Sherman
PPLICANT: Gao, Wai-Qiang
PLICANT: Gao, Wai-Qiang
PLICANT: Goodward, A. Licant:
CANT: Goodward, Austin L.
CANT: Grimaldi, Christopher J.
CANT: Grimaldi, Christopher J.
CANT: Mather, James
VIT: Ray, Austin L.
CANT: Mather, James
VIT: Paoni, Nicholas F.
T: Roy, Margaret Ann
Stewart, Timethy A.
THUMS, Daniel
Williams. Timethy A.
Tumas, Daniel RESULT 1
US-09-907-794A-169
i Sequence 169, Application US/09907794A
parent No. 6635468
GENERAL INFORMATION:

SUMMARIES

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued_Patents_NA:*
1: /cgn2 &/ptodate2/lina/5A_COMB.seq:*
2: /cgn2 &/ptodate2/lina/5B_COMB.seq:*
3: /cgn2 &/ptodate3/lina/6A_COMB.seq:*
4: /cgn2 &/ptodate3/lina/6B_COMB.seq:*
5: /cgn2 &/ptodate3/lina/PCTUS_COMB.seq:*
6: /cgn2 &/ptodate3/lina/PCTUS_COMB.seq:*

Database :

Description	enc	Sequence 169, App	Sequence 169, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	H	Sequence 603, App	Sequence 22, Appl		24,	Seguence 3, Appli
ΙD	US-09-907-794A-169	US-09-905-125A-169	US-09-902-775A-169	US-09-181-706-1	US-09-458-791-1	US-09-459-066-1	US-09-459-065-1	US-09-023-655-603	US-08-306-691B-22	PCT-US93-06251-27	US-09-300-958A-24	US-09-077-940A-3
80	4	4	4	m	m	m	4	41	-	Ŋ	4,	4
% Query Match Length DB	2477	2477	2477	4707	4707	4707	4707	3458	4626	4626	2433	3524
% Query Match	13.6	13.6	13.6	13.5	13.5	13.5	13.5	9.9	6.3	6.3	3.2	5.6
Score	1359.5	1359.5	1359.5	1349	1349	1349	1349	657	629.5	629.5	323	263
Result No.	Н	7	m	4	2	9	7	80	σ,	10	11	12

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                  |AsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAspLysLe
                                                                                                                       tValSerProProGly------SerThrThrLysGluGlnValTyrThrSerLysLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PLING DATE: 1999-07-26
PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-29
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-07
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1359.50
69.88%
53.35%
13.61%
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CORGANISM: Homo sapiens
US-09-907-794A-169
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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460 jAspGlyProArgGlyAsnAlaLeuGlnTyrGlu------ThrValGlnVa

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103 rCysAsnGluProLeuThrThrAsnAsnValAsnLysMetLeuLeuIeAspTyrLy 123

rHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArg1leValGlnTh 103

TCATAAGACCCAGAAGAAGACAACAAGAAGTCTCGTTACCCGCCCTCATCGTGCAGCC

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                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION NUMBER: PCT/US99/30999;
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219;
PRIOR PILING DATE: 2000-01-05;
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 169
LENGTH: 2477
TYPE: DNA
ORGANISM: Homo sapiens
US-09-905-125A-169
                                                                                                                       8.8e-138
1359.50
69.88%
53.35%
13.61%
                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                               Alignment Scores:
Pred. No.:
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                                                                                                               CACCCGGGCCGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGA 1787
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                                                                                                                                                                                                                                                     uLysGlnileAsnAspArgileLysGluArgLeuGlnSerCysTyrArgGlyGluGlyTh 380
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                                                                                                sGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAl 320
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---SerThrThrLysGluGlnValTyrThrSerLysLe 280
                                                                                                                                                                                                                                                                                                                    eAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValAr
                                                                                                                                                                                                                                                                                                                                                                                                                     2148 CAACGGCTACAGGGTTTTTTGTGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 lAspGlyProArgGlyAsnAlaLeuGlnfyrGlu------ThrValGlnVa
                                                                                                                                                                                                                                                                                                                                                                                                       420 gGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrValTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 lValAspProGlyProValLeuArgAspMetAlaPheSerLys---AspHisGluGlnLe
                  1612 ----ACCCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCAT
                                                uValArgLeuCysLysGluAspThrAlaPheAsnSerTyrValGluValProlleGlyCy
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263 tValSerProProGly.
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Pan, James Paoni, Nicholas F.

Fong, Sherman
Gao, Wel-Qiang
Garber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J. RESULT 3
US-09-902-775A-169
US-09-902-775A-169
Sequence 169, Application US/09902775A
Patent No. 668451
GENERAL INFORMATION: Ferrara, Napoleone Filvaroff, Ellen APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Betstein, David
APPLICANT: Baton, Dan L.
APPLICANT: Baton, Dan L.
APPLICANT: Fivaroff, Ellen
APPLICANT: Fivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, A.

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------GGCCCCCCCAGCAGCCATGCCTCAGTTCAGCACCTTCCA 953
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                                                                                                                                                                                                 Transmembrane Polypeptides and Nucleic
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Matches:
Conservative:
Mismatches:
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timethy A.
APPLICANT: Stewart, Timethy A.
APPLICANT: Wood, William, F. Mickey
TITLE OF INVENTION: Secreted and Transmembrane P
TITLE OF INVENTION: Acids Encoding the Same
PILOR APPLICATION NUMBER: US/09/902,775A
CURRENT APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-08
PRIOR PLING DATE: 1999-09-18
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
PRIOR PLING DATE: 1999-12-03
PRIOR PLING DATE: 2000-01-05
PRIOR PLING DATE: 2000-01-05
PRIOR DATE: 2000-01-05
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53.35%
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; ORGANISM: Homo sapiens
US-09-902-775A-169
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Best Local Similarity:
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DD 2028 CGATGATTCTGTGGATGGACATCAGCCGCCCGATGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGGACTGCATGGACTGCATGGACTGCACCCCCCCC	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/181,706 FILING DATE: October 28, 1998 CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: Provisional, see below FILING DATE: October 28, 1997 CLASSIFICATION: PRIOR APPLICATION NUMBER: Provision to Provisional APPLICATION NUMBER: Conversion to Provisional APPLICATION NUMBER: Conversion to Provisional APPLICATION NUMBER: Conversion to Provisional APPLICATION NUMBER: 34,347 FILING DATE: October 26, 1998 CLASSIFICATION NUMBER: 34,347 ATTORNET, ABTS CONTONING CONTONING NUMBER: 34,347 REGISTRATION NUMBER: 34,347 REGISTRATION NUMBER: 34,347 REGISTRATION NUMBER: 2631-A TELEPHONE: (2061470-4189 TELEPHONE: (206123-0644 INFORMATION FOR EEQ ID NO: 1: SECURENCE CHARRATTERISTICS: LENGTH: 4707 base pairs TYPE: NUMBER: double STRANDEDNESS: double STRANDEDNESS: double STRANDEDNESS: double
49 GG1yG1uProhlaG1uG1yPhaksnBisteuvalValkspolukrgfhrG1yHis11 63 52 CTCTGAGAATCGTGACTGACCACTTGACGACCAGGGGGGCCT 1013 53 FTYLEuG1yAlaValksnActGACTTGACGACCACCAGGGGGGGCCT 1013 54 CTCTGAGAATCGTGACTGACCACTTGACGACCACCAGGGGGGCCT 1013 55 FTYLEuG1yAlaValksnActGACTGACGACCACCAGGGGGGCCT 1013 56 FTYLEuG1yAlaValksnActGACTGACGACCACCAGCCAGGGGGCCT 1013 57 FTATAGACAGGGCCAGAAGGACACACACACACGACCGACCTGACCACTGACCAGGGGCCAGGGGCAGAAGGACACACAC	1612ACCCCTGAGGGTGTGGCCATCAACTCGGCTGGAGGCCTTCTCTACACCCCACGCAT 1667 280 UVAlAEGGTGTGGCCATCAACTCGGCTGGAGCCTTTCTACACCCCACGCAT 1667 1668 CGTGGGGCTCTGCAAGGATGACCCCAAGTTCCACTCATACCTGCCCTTCGGCTG 1727 300 SGTUATGSGCTCTGCAAGGATGACCCCAAGTTCCACTCATACCTGGCCTTCGGCTG 1727 300 SGTUATGSGCTGTGAACTACCCCCAAGTTCCACTCATACCTGGCCTTCGGCTG 1727 310 SGTUATGSGCTGTGAAATACCCCCTCCAAGGCTGCTTACCTGGCCAAGCTGGCAAGTTACTTGGCTGGC
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; HYPOTHETICAL: NO ; ANTI-SENSE: NO ; FEATURE: ; NAME/KEY: CDS ; LOCATION: 1..4707 US-09-181-706-1

Alignment Scores:

	A 119 ment Scores Score: Score: Score: Serional Similar Best Local Similar Ouery Match: DB: Cy	### ### ##############################	1147; 1349:00 Mat 1349:00 Mat 1349:00 Mat 139:78 Mis 13:78 Mis 13:50 Mis 13:50 Mis 14:1896 X US-09-181-706- 14 15 16 16 16 17:18196 X US-09-181-706- 16 17:18196 X US-09-181-706- 18 18 19 10 10 10 11	1349.00 Matches	### ### ##############################	
S S	158 436	HisTyrLeus TCCCTGCGCA	Serglyval : : Aacggcaccgaggrg	AsnGluSerGl 	ySerValPheGlyVal 17	
S S	173	Ilevalser ::: GTGTACCGC	17t	erAsnLeuAspAspLysLeuPheIleAl :: ::::::: ::::::::::::::::::::::::	SerasnLeuAspAspLysLeuPheIleala	
9 S	187	CTGCCTGAG	CCGGAGACGGCGAGC	CGCTGCAACCCCGCGCG	CTGCCTGAGCCGGAGAGCGGCTGCAACCCCGCGGGCATCCGACCACGACACGGCC 612	
रेठ व	189	ValAspGlyLy ::: ATCGCGCTCAA	LysProGluTyrPheProThrIl adGaCaCGGAGGGCGCAGCCT	ProThrIleSerSerA ::::::::::::::::::::::::::::::::::::	AspGlyIysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208 	
Sp G	209	Glualaasp ::: CTGTGCGAG	aAspGlyMetPheAlaTyrValPheHi ::: CGAGGGGGGGAGCTGCACTTCGT	ValPheHisAspGluPheV : CACTTCGTGGACGCCTTTC	GlualaAspGlyMetPhealaTyrValpheHisAspGluPheValAlaSerMetIle 227 :::	
ò g	228	LysilePro TACTTCCCC	eProSerAspThrPheThrIl CCCC	IleileProAspPheAspil	ASDIJETYTYTVAJTYTGJY 247	
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λ O	268	GlyserThr CAGAGCACC	ThrLysGluGlnVal	TyrThrSerLysLeuV	TYrThrSerLysLeuValArgLeuCysLysGluAsp 287 ::: :::	
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307	TyrArgicuLeuGinAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu 326
2	GlvValHisproAspAspAspLenLenPheThrValPheSer1wsGlvGlniws 34.
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345 952	ArglysMetLysSerLeuAspGluSerAlaLeuCysIlePhelleLeuLysGlnIleAsn 364 ::::: ::
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385	TrpLeuLysValLysAspileProCysSerSerAlaLeuLeuThrI
1072	AspMetValArgGlyI
10	alPheThrGluAspArgAspArgMetThrServallleAlaTyrValTyrLySAsnHis 443
1162	12
464	GAAGAGACA 12
491	ÖΕ
511	GlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCys 530 ::::::::
531	ValleuHisAsnThrCysThrArgLysGluArgCysGluArgSerLysGluProArgArg 550
551	eAlaSerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIlsSerVal 570
1462	rGlamrebontaltontontaltonGlambetrandantalbonglatonGaranala
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591	Leus
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611	GlnCysTyrSerProAlaAlaLysGluValProArgIlelleThrGluAsnGlyAspHis 630
631	isvalvalGlnL
1 10	PheTyrAsnCysSerValHisAsnSerCysLeuSerCysValGluSerPro 669

tAlaArgValGlyGlyMetGluTyrSer 1222 :::::||| :::||| GGTCAAGCTGGAAACCTGGAG----- 2799 rProllelleLeuLysGlyLysAsnLeu 1168 AgnTyrThrValLeuValGlyGluLys 1188 |||| ::: |TCCTTCCACATGGTATTTTCTGATTGTG 2850 -IleProPheLeuAspTyrArgThrTyr 1320 :::||||||||||||| rGTTCCTTCTTGACTACAAACATTT 3063 eGluAspHisProvalLeuArgAspLeu 1338 |||| |CTTCACCCACATCTTCACTGAAGATATG 3123 illeCysgluValLeuAsnAlaThrGlu 1093 ProAspHisGlnSerAspLeuThrGlu 1113 NajGlnSerLeuLeulleLeLeuAsnLys 1133 ||||| |GTCACTGTGAAGCTGAGAGTACAAGAC 2490 oArgAlaLysIleHisGlnAspLeuVal 1033 GGTGGGAACTGCTCTTCTGTGGGATCC 2241 TTCTCTCTTCCATCAGCCGGAAA--- 2184 -ProLeuSerLeuProAlaIleValSer **TTGCAAAATTAAAGGCATCAAGACTGCA** JILEGLUPROGLUTRDSERILEVALSER

us-09-964-956-13.rni

TELEPHONE: (206)470-4189
TELEPKA: (206)23-0644
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE: NAME/KEY: CDS LOCATION: 1..4707 SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-458-791-1

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 4.26e-136 1349.00 39.78% 24.77% 13.50% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
3

Alignment Scores: Pred. No.:

4707 480 291 591 576

US-09-964-956-13 (1-1896) x US-09-458-791-1 (1-4707)

340 GAGGGGGGGGCGGCCTCGGGGGGGCTGCTGCTCGGCTGGACCTTCGACCGGGGGGCCC 399 172 ::: ||| ::: ||| | ::: || || | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || | ::: || ::: || | ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || :: 209 GlualaAspGlyMetPheAlaTyrValPheHisAspGluPheVal---AlaSerMetIle 227 TACTTCCCC----TACTACCCCTACAC 756 248 PheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerProPro 267 256 ---------AACTGCACAGAGCCGGTCTCGCTGGCG 282 123 283 CCCCCGGGGGGCCCCGGGAGCAGCTTCAGCAAG---CTGCTGCTGCTACCGC 339 138 CysLysLeuLeuArgleuGluAspleuPheLysLeuGlyGluProTyrHisLysLysGlu 157 400 TGCGAGGTGCGGCCCCTGGGCAACCTG------AGCCGCAAC 435 173 IleValSerTyrSerAsnLeuAspAspLysLeuPheIleAla--------- 186 187 -------ThrAla 188 189 ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208 673 crereceaededecesecaeccrecacirderedadeccriricreresaacescaecare 732 228 LysileProSerAspIhrPheThrileileProAspPheAspIleTyrTyrValTyrGly 247 111 91 72 TyrLysLeuSerSerAspLeuLysValLeuValThrHisGluThrGlyProAspGluAsp 208 hacagecrasagecracitates de la recessa de 92 AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThr 158 HisTyrLeuSerGlyVal-------AsnGluSerGlySerValPheGlyVal ò g ò qq 8 6 8 \$ 8 \$

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757	TATACGAGCGGCGCTGCCACCGGCTGGCCCAACATGGCGCGCATCGCG 804
268	GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAsp 287
805	CAGAGCACCGAG 816
288	AsnSerTyrValGluValProlleGlyCysGluArgSerGlyValGlu 3
817	danggachagcarccragacradagcacchagachaga
307	TyrargleuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu 326
20 0	lyValHisProAspAspAspLeuLeul
,	LiddACGLC1C1GGGGGGGGGGGTTCAGCGGCGGGCGGCGGGGGGGGGG
345 952	2
9	hrgilelysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeuAspLeuAla 384
1012	GCGCCAAGAGGGTCAGC 10
385	TrpLeuLygValLygAsplleProCysSerSerAlaLeuLeuThrlleAspAspAsn 403
404	eCysGlyLeuAspMetAsnAlaProLeuGlyValS
1072	GAAAGAGTCCAACCAATCG
424	ValPheThrGluAspArgAspArgMetThrSerVallleAlaTyrValTyrLysAsnHis 443
7110	TACCITEALCCALICCEACCIEACAICCEILIAIGECACCEIGEIANIGANCAGE TIG
1162	SerLeualaPheValGlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyPro 463::
464	ArgGlyAsnAlaLeuGlnTyrGluThrValGlnVal
1213	GGTGAGAATTTGACTTCAAATTGTCCAGAGGTTATCTATGAAATTAAAGAAGAGACA 1269
477	gAsj
1270	CCTGTTTTCTACAAACTCGTTCCTGATCCTGTGAAG 1305
491	II 4
511	GlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCys 530
1366	
531	ValleuHisAsnThrCysThrArgLysGluArgCysGluArgSerL
1426	CATICGCI
551	PheAlaSerGluMetLysGlnCysValAr
1462	GLACAT
571	SerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGly 590
1483	AACTGGCTGGATATTTCGTCTGGA 15
591	ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610
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δγ	611 GlnCysTyrSerProAlaAlaLysGluValProArgIleIleThrGluAsnGlyAspHis 630	
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qq	1528CAGATAATTCGAAGCAGTAAAGAAAAGACTACAGTGACTATGGTGGGAAGC 1578	
ζλ	651 PheValPheTyrAsnCysSerValHisAsnSerCysLeuSerCysValGluSerPro 669	
qq	AAAGTGC	
λά	670 TyrargCysHisTrpCysLysTyrArgHisValCysThrHisAspProLysThrCysSer 689	
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λά	690 PheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAspLys 709	
qo	1638 1638	
λ	710 IleLeuValProValGluValIleLysProlleThrLeuLysAlaLysAsnLeuProGln 729	
qq	1639CAGAATAAAAGTCAG 1653	
٥'n	730 ProGlnSerGlyGlnArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArg 749	
qq	1654 CCCAACGG 1680	
λ̈́ο	750 ValProAlaLeuArgPheAsnSerSerSerValGlnCysGlnAsnThrSerTyrSerTyr 769	
QQ	1681CCAACCAGAGCAACCTACAAGATGTTTCAGTTGTCAACGTGATGTTCTCCTTC 1734	
λ̈́O	770 GluGlyMetGlulleAsnAsnLeuProValGluLeuThrValValTrpAsnGly 787	
QQ	1735 GGTTCTTGGAATTTATCAGAC 1755	
ò	788 HisPheAsnIleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMet 807	
Db	1756 AGATTCAACTTTACCAACTGCTCATCATTA 1785	
ζ	808 ArgGluSerCysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGln 827	
QQ	1786 AAAGAATGCCCAGCATGCGTAGAAACTGGCTGCGCGTGGTGTAAA 1830	
ογ	828 GlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGlu 847	
Db	1831 AGTGCAAGAAGATGT 1845	
٥٨	848 LeuSerGlyAlaLysSerLysCysThrAsnProArglleThrGlullelleProValThr 867	
Db	1846ATCCACCCTTCACA 1860	
ò	868 GlyProArgGluGlyGlyThrLygValThrIleArgGlyGluAsnLeuGlyLeuGluPhe 887	
qq	1861 GCT 1863	
ζ	888 ArgAspileAlaSerHisValLysValAlaGlyValGluCysSerProLeuValAspGly 907	
Db	1864TCT 1875	
δ	908 TyrileProAlaGluGinileValCysGluMetGlyGluAla 921	
qq		
λŏ	922 LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPhe 941	
Db	1936 AGACCCCAAGGAGAACAAGGGGAACAGA 1962	
٥٧	942 MetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysPro 961	
Db	1963 ACCAACCAGGTTTACAGGTCTTCTACATTAAGTCCATTGAGCCA 2007	

96	981	
2008	AAGTATCGACATTAGGGAAAAGCAACGTGATAGTAACGGGAGCAAACTTTACCCGG Z	
982 2068	GlyserasnvalvalvalmetPheGlyLysGlnProCys 994 ::: :::::::: ::: ::::::::	
995 2128	LeuPheHisArgArgSerProSerTyrIleValCysAsnThrThrSerSerAspGluVal 1014	
1015	LeuGluMetLysValSerValGlnValAspArgAlaLysIleHisGlnAspLeuVal 1033 	
1034	PheGlnTyrValGluAspProThrIleValArglleGluProGluTrpSerIleValSer 1053	
1054	GlyasnThrProilealaValTrpGlyThrHisLeuaspLeuileGlnAsnProGlnIle 1073	
1074	ArgalalyshisglyglyLysgluHisIleasnIleCysGluValLeuAsnAlaThrGlu 1093	
1094	MetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGlu 1113 TGCGGGTTTTTAGCCCCCAGTTTA2439	
1114	ArgProGluGluPheGlyPheIleLeuaspAsnValGlnSerLeuleuIeLeuAsnLys 1133 ::: ::: :::	
1134	ThrAenPheThrTyrFyrProAenPredIpheGluAlaPheGly 1148	
1149	ProSerGlyIleLeuGluLeuLysProGlyThrProIleIleLeuLysGlyLysAsnLeu 1168 GTGGAATCCGAGGTGGACACAGAACTGGAAGTGAAAATTCAA 2592	
1169 2593	IleProProValAlaGlyGlyAsnValLysLeuAsnTyrThrValLeuValGlyGluLys 1188	
1189	ProCysThrValThrValSerAspValGlnLeuLeuCysGluSerProAsn 1205	
20	120	
2686	ATTACTAGAAATCAAGATCTTACCACCATCCTTTGCAAAATTAAAGGCATCAAGACTGGC 274	
1208	GlyArgHisLysValMetAlaArgValGlyGlyMetGluTyrSer 1222 AGCACCATTGCCAACTCTTCTAAGAAGTTCGGGTCAAGCTGGGAAACCTGGAG 2799	
1223		
1242	IlealavalalaGlyGlyLeuLeuIleIlePheIleValalaValLeuIleAlaTyTLys 1261 :::	
1262	ArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnLeu 128 :::	
1282	GluSerArgValAlaLeuGluCysLygGluAlaPheAlaGluLeuGlnThrAgpIleHis 1301	

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MetAsnAlaTyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrMetSer 1848
                                                                                                                                                                LeuProLeuAlaileiyeTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGly 1728
                                                                                                                                                                                                                                                                                                                            GCCTGTTTGTCAGTGATTGCCCAGGCATTCATGGATGCATTTTTCTCTCACAGAGCAGCAA 4377
                      MetTrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGlySer 1670
                                                                                                                     GlnLysPheValAspAspLeuPheGluThrilePheSerThrAlaHisArgGlySerAla 1708
                                                                    GAAGAAGTAAAATCTTATTACAAAGCAATCAGGGATTTGCCTCCATTGTCATCCTCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1849 AlaLeuSerGluilePheSerTyrValGlyLysTyrSerGluGluileLeuGlyProLeu
                                                                                                                                                                                                               | IleHisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrp
                                                                                                                                                                                                                                                               ValAsnMetIleLysAsnProGlnPheValPheAspIleHisLysAsnSerIleThrAsp
                                                                                                                                                                                                                                                                              1769 AlaCysLeuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArg
                                                                                                                                                                                                                                                                                                                                                                                                          1809 AsnTrpValGluArgTyrTyrSerAspileGlyLysMetProAlaIleSerAspGlnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTCTGTGCTTGAAAAACTTTTTAGAAGCATTTGGAGTTTACCCAAC----AGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1869 AspHisAsp-----AspGlnCysGlyLysGlnLysLeuAlaTyrLysLeu 1883
 GTGGAGTACTCGGATGACCACTGCCATTTGATTTTACCAGATTCGGAAGCA-
                                               ---TTCCAAGATGTGCAAGGAAAGAGACAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProAspSerLeuArgSerArgThrProMetIleThrProAspLeuGluSerGlyValLys 1650 :::
                                                                                                                                                                                                                                                                                                                                                  3405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrThrLyslleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisTyrGlnValPro 1590
                                                                                                                                                                                                                                                                                                                                                                                                                       ProLeuPheSerLeuPheCysAlaIleLysGlnGlnMetGluLysGlyProIleAspAla 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1477 ileThrGlyGluAlaArgTyrSerLeuSerGluAspLysLeuIleArgGlnGlnIleAsp 1496
||||||| ::: |||| || GAAAGCGAGGAAAGAGAAAAAATTG 3012
                                                                                                                                GluValProGlyTyrArgGlnGluArgValGluLysGlyLeuLysLeuPheAla---- 1356
                                                                                                                                               LysteuGluTyrAlaThrAspValLeuLysGlnLeuLeuAlaAspLeulleAspLysAsn 1416
                                                                                                         3064 GCTCTGAGAACTTTCTTCCCTGAGTCAGGTGGCTTCACCCACATCTTCACTGAAGATATG 3123
                                                                                                                                                                                             -----AGTAACATGCAGCCGAAACTCATGCTGAGACGCACGGAGTCCGTCGTCGTCGTCGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                        3406 CICCICACAAACIGGAIGICGCTTITCIGGAITITCICGGGAGACIGICGGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetAspleuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1417 LeuGluSerLysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLys
                                                                                                                                                                                                                                                                                                                                                                         MetheuThrasnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                               3586 TICAGTACTGTGGCATTAAACGTCGTCTTTGAAAAATCCCCGGAAAACGAGAGTGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GluValProValLysIleLeuAsnCysAspThrileThrGlnValLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspGlySerValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaValAsnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------TTTAAGAAGATAGCAAATTTTÄĊŤTCAGAT
                                                                                                                                                                              GlnLeuIleAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArg
                                                                                                                                                                                                                              SerPheSerMetArgAspArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSer
                                                                                                                                                                                                                                                                                           TyrLysThrLeuValLeuSerCysVal -----SerProAspAsnAlaAsnSerPro
                                   GluLeuThrSerAspLeuAspGlyAlaGly---IleProPheLeuAspTyrArgThrTyr
                                                  ThrMetArgValLeuPhePro-----GlyIleGluAspHisProValLeuArgAspLeu
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RESULT 6

US-09-459-066-1

US-09-459-066-1

Patent No. 618709

Patent No. 618709

Patent No. 618709

TITLE OF INVENTION:

TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Janis C. Henry

STREET: 51 University St.

CITY: Seattle

STATE: WA

COUNTRY: US

TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

STREET: 51 University St.

CITY: Seattle

STATE: WA

TO COUNTRY: US
```

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/958,598

FILING DATE:

NAME: Henry, Jania C

REGISTRATION NUMBER: 34,347

REFERENCE/DOCKET NUMBER: 2631

TELEPHONE: (206)470-4189

TELEPHONE: (206)470-4189

TELEPHONE: (206)23-0644

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4707 base pairs

TYPE: NUMBER: caid

STRANDEDNESS: double

MOLECULE TYPE: CDN

HYPOTHETICAL: NO

ANTI-SENSE: NO

RANTI-SENSE: NO

RANTI-SENSE: NO

NAME/KEY: CDS

LOCATION: 1.4707

US-09-459-066-1

4707 480 291 591 576 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: Alignment Scores:

Pred. No.:
Score:
1 Percent Similarity:
Best Local Similarity:
2 Query Match:
1 Best

US-09-964-956-13		(1-1896) x US-09-459-066-1 (1-4707)	
ζ	72 Tyr]	roAspGluAsp	91
QQ	208 TAC	208 TACAGCCTGGAGCACAGCCTCTCGCGCCTGTACCGGGACCAAGCGGGC22	255
ργ	92 Asnl		111
QQ	256	AACTGCACAGAGCCGGTCTGGCG 2:	282
ò	112		123
qq	283 000	CCCCCGCGCGCCCCGGGGGGGAGCAGCTTCAGCAAGCTGCTGCTGCTCTACCGC 3.	339
δγ	124 Glu		137
qq	340 GAG	GAGGGGGGGGCGTCGGGGGGCTGCTGACCGGCTGGACCTTCGACCGGGGGCCC 3	39
۵,	138 Cys]	LysLeuGlyGluProTyrHisLysLysGlu	157
qq	400 TGC	TGCGAGGTGCGGCCCCTGGGCAACCTGAGCGGCAAC 4	435
δŻ	158 His'		172
qq	436 TCC	TCCCTGCGCAACGGCACCGAGGTGGTCGTGCCACCCGCAGGGCTCGACGGCCGGC	495
ò	173 Ile		186
QQ	496 GTG	GIGTACCGCGCGGGCCGGAACCACGCTGGTACCTGGCGGTGGCCGCCACCTACGTG 5	552
δλ	187	Thrala 1	188
Dp	553 CTG	CTGCCTGAGCCGGAGCGGCGGCTGCAACCCCGGGGCATCCGACCACGACGGGCC 6	612
ζ	189 Val.		208
qa	613 ATC	ATCGCGCTCAAGGACAGGGGGGGGGGGCTGGCTGGCAGGAGCTGGGGGGGCGCCTCAAG 6	672
8	209 Glu	209 GlualaaspGlyMetPheAlaTyrValPheHisAspGluPheValAlaSerWetIle 2	227

673	ctgracaagacacaacaaccracactrcaraaacaacaacaacaacaacaacaacaacaacaacaa
228	LysileProSerAspThrPheThrileileProAspPheAspileTyrTyrValTyrGly 247
733	CTACTACCCTA
4, 1	alTyrPheLeuThrLeuGlnBroGluMetValSerProPro 26
L)	GCTGCCACCAGCTGGCCCAGCATGGCGCGCATCGCG 80
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-	GUIGITUCAGGCCAGGCAICCITGACIGCGGCCACGGCCACCACGACGGC 8/
307	TyrArgLeuleuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu 326 ::::: ::: ngcngcmgcmccmncrmcrancangacmangangangangac
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365	AspargilelyşGluArgLeuGinSerCysTyrArgGlyGluGlyThrLeuAspLeuAla 384
1012	 CAAGAGG
385	rpLeulysvallysAsplleProCysSerSerAlaLeuLeuThrlleAspAsn 403
1033	CGAGAGCCA
404	Se
1072	– F
424	ValPheThrGluAspArgAspArgMetThrSerVallleAlaTyrValTyrLysAsnHis 443
1102	
444	SerLeuAlapheValGlyThriysSerGjyLysLeuLysLysIleArgValAspGlyPro 463
1162	ACTGTTTTATTCT
464	ArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVal
1213	GAATT
477	AspProGlyProValLeuArgAspMetAlaPheSerLysAsp 490
1270	CCTGTTTTCTACAAACTCGTTCCTGATCCTGTGAAG 1305
491	HisGluGlnLeuTyr11eMetSerGluArgGlnLeuThrArgValProValGluSerCys 510
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511	GLYGLITYYGLISSECV8GLYGLUCYSLEUGLYSEZGLYASPPYOHISCY8GLYITDCYS 530 s:::::
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1426	VAILEUHISASSITOTVATOTARIGLYSSILUARGSSELVSSULUKIOALGALG 330
551	PheAlaSerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIleSerVal 570
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922 Ly8F ::: 1936 AGA 942 Meth 1963 ACCA 962 SerA	982 Gly6 2068 GCA1 995 LeuE 2128 GITE 1015 LeuG 2185G			2626 GAC 1206 Leu 1206 Leu 1208 1208 2746 AGC 1223 Proc 2800
6 6 6 6 6	6 8 6 8 6	8 8 8 8 8 8 8	3 8 5 8 5 8 5 8 5 8	\$ A & A & A & A
1462	HisvalvalGinLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSer	690 PheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAspLys 709 1638		848 LeuSerGlyAlaLysSerLysCysThrAsnProArgileThrGluileIleProValThr
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JGluMetLys---ValSerValGlnValAspArgAlaLysIleHisGlnAspLeuVal 1033 tThrCysGlnAjaproAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGlu 1113 gProGluGluPheGlyPheIleLeuAspAsnyalGlnSerLeuLeuleulleLeuAsnLys 1133 r------AsnPheThrTyrTyrProAsnProValpheGluAlaPheGly 1148 oSerGlylleLeudjuLeuLysProGlyThrProllelleLeuLysGlyLysAsnLeu 1168 eProProValAlaGlyGlyAsnValLysLeuAsnTyrThrValLeuValGlyGluLys 1188 . TACTAGAAATCAAGATCTTACCACCATCCTTTGCAAAATTAAAGGCATCAAGACTGCA 2745 ------GlyArgHisLysValMetAlaArgValGlyGlyMetGluTyrSer 1222 oGlyMetValTyrIleAlaProAspSer---ProLeuSerLeuProAlaIleValSer 1241 PheHisArgArgSerProSerTyrIleValCysAsnThrThrSerSerAspGluVal 1014 eGlnryrvalGluAspProThrIleValArgijeGluProGluTrpSerIleValSer 1053 AsnThrProileAlaValTrpGlyThrHisLeuAspLeuileGlnAsnProGlnIle 1073 gAlaLysHisGlyGlyLyksGluHisileAsnIleCysGluValLeuAsnAlaThrGlu 1093 oCysThrValThrVal-----SerAspValGlnLeuLeuCysGluSerProAsn 1205 :::|||::: -----CTCTACGTCGAGCAGTCAGTTCCTTCCACAIGGTATTTTCTGATTGTG 2850 ----AACAGA 1962 |||||||||| ATCGAACATCACAATGATCCTGAAAGGAACCAGTACCTGTGATAAGGATGTGATACAG 2127 sproSerGlnHisAlaGlyPheValGlulleCysValAlaValCysArgProGluPhe 941 rArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAla 981 -GAAATGAAGGATGTGTGTATCCAGTTTGATGGTGGGAACTGCTCTTCTGTGGGATCC catttcacaigaattaaaaggaaacaiaaaigtctctgaatattgtgtgggggcitac /SerAsnVal---ValValMetPheGlyLysGlnProCys------CGGGTTTTTAGCCCCCAGTTTA-----

Page 14

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v	
1242 IlealavalaladlyGlyLeuLeulleIlePheileValalavalLeulleAlaTyLys 1261 :::	GIUVALPECGIAGATTCTTCCCTGAGTGGGTTCACCCACATTTCACTGAAGATATG 112 GIUVALPECGIAGATTTCTTCCCTGAGTGGGTTCACCCACATTTCACTGAAGATATG 112 GIUVALPECGIAGATTTCTTCCCTGAGTGGGTTCACCCACACTTTCACTGAAAGATATG 112 GIUVALPECGIAGATTTCTTCCCTGAGTGGTTCACTTCACCCACACTTTCACTGAAAGATATG 112 GIUVALPECGIAGATTACTTCCTTGATACACACACACACACACACTTCCACACGTTTGGAT 117 GINLeulleAsnAsnLysValPheleuLeuSerbeileArgThrLeuGluSerGlnArg 1137 GCCCTAATCTGTAATAAAACTTTCTTGTTACTGTCACACACA
	3 B S

Db 388 Qy 161 Qy 165 Qy 165 Qy 177 Qy 177 Qy 177 Qy 184 Qy 177 Qy 186 Qy 177 Db 443 Qy 177 Db 445 Qy 117 Cy 188 Cy 177 Db 445 Cy 188	1 SerThrValSerArgThrSerAlaSerLysTyrGl		11 ProAspSerLeuArgSerArgThrProMetlleThrProAspLeuGluSerGlyValLys 1650	MetTrpHisLeuValLysAsnHisGluHisGlyAspGlnLysGluGlyAspArgGlySer 16		1 LysMetValSerGlulleTyrLeuThrArgLeuLeuAlaThrLysGlyThrL	4 CACAAGTTCAAAGTAAAAGAAATGTATCTGACAAAGCTGCTGTCGACCAAGGTGGCAATT 4083	9 GlnLysPheValAspAsp	84 CATTCTGTGCTTGAAAAACTTTTTAGAAGCATTTGGAGTTTACCCAACAGCAGA 4137)9 LeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGly 1728	9 IleHisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrp 174		9 ValAsnMet	8 GTAAACATCCTGAAGAACCC	19 AlaCysLeuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArg 1788	9 LeuGlyLysAapSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLys 18		9 ABnTrpValGluArgTyrTyrSerAspileGlyLysMetProAlaileSerAspGln	88 GAAGAAGTAAAATCTTATTACAAAGCAATCAGGATTTGCCTCCATTGTCATCCTCAGAA 4497	99 MetasnalaTyrieualaGluGlnSerArgMetHisMetasnGluPheAsnThrMetSer 1848 	9 AlaLeuSerGluile	:: ::: 8 GCCTTGACAGAAATTTACAAATACATCGTAAAATATTTTGATGAGATTCTAAATAAA	AspGlnCysGlyLysGlnLysLeuAlaTyrLysLeu 1	GARAGABARACANGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	
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COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Word for Windows 95, 7.0a
APPLICATION NUMBER: US/09/459,065
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 08/958,598
FILING DATE:
APPLICATION NUMBER: 34,347
REPERIOR APPLICATION INDER: 2631
FILING DATE:
ATORNEY/AGENT IRFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 2631
TELECHONE: (206/470-4189
TELECHONE (206/470-4189
TELECHONE (206/470-4189
TELECHONE CHARACTERISTICS:
LENGTH: 4707 base pairs
TYPE: nucleic acid
STRANDENESS: double
TYPE: nucleic acid
STRANDENESS: double
TYPE: NO
ANTI-SENSE: NO
REATURE:
NAME/KEY: CDS
NAME/KEY: CDS

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TR-04-404-400-TO-BH

TIT WGY 40 TO:45:45 400%

 US-09-459-065-1
 Alignment Scores:
 4.26e-136
 Length:
 4707

 Pered: No.:
 1349,00
 Conservative:
 291

 Percent Similarity:
 39.78*
 Conservative:
 291

 Best Local Similarity:
 24.77*
 Mismatches:
 591

 Query Match:
 4
 74

 DB:
 74

US-09-964-956-13 (1-1896) x US-09-459-065-1 (1-4707)

187		D
553	CTGCCTGAGCCGGAGACGGCGAGCCGCTGCAACCCCCGCGGCATCCGACCACGACACGGGCC 612	C)
	ValAspGlyLysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSer 208	00 (
613	GCTCAAGGACACGGAGGGGCACCTGGCCACGCAGGAGCTGGGGGCCCCTCAAG	N 1
209	GlualaspGiyMetPheAlaTyrValPheHlsAspGuluPheValAlaberMetlle 22/ i::	- 0
23	ProAspPheAspIleTyrTyrValTyrGly 24	,
m ·	TACTTCCCCTACTACCCCTACAA	
757	PRESENTATION OF THE PRINCIPLE OF THE POSITION	- 4
. 268	GlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGluAsp 28'	r 4
· 00	ThralapheasnSerTvrValGluValProlleGlvCvsGluArgSerGlvValGlu 30	
	GTGCTGTTCCAGGGCCAGGCATCCCTCGACTGCGGCCACGGCCACGGC 87	
307	TyrargheuleudlnalaalaTyrheuSerbysalaGlyalaValleuGlyargThrLeu 32	
871	CGCCGCCTGCTCCTCCTCCAGCCTAGTGGAGGCC	
327	GlyvalHisProAspAspLeuLeuPheThrValPhSerLysGlydluLys 34.	4 4
345	ArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsn 36:	4 1
36	AsparglleLysGluargLeuGlnSerCysTyrargGlyGluGlyThrLeuaspLeuala 38	5 14 (
1012	GCGCGCGCCAAGAGGGTCAGC	m m
385	TrpbeulygvallygasplleProCysSerSerAlaLeuLeuThrlleAspAspAsn 40	5 7
404	PheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetValArgGly1lePro 42	უ ნ
1072		9 19
1102	VALFNEHINGLUASPANGASPANGAS VALLESTATIVE TATIVET TO THE TOTAL THE TO	, [6
444	SerLeuAlaPheValGlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyPro 46	m
1162	ACTGTTTTATTCTTGGGGACTGGAGATGGCCAGTTACTTAAGGTTATTCTT 12	7
464	ArggiyasnalaLeuGlnTyrGluThrValGlnValVal	9 9
477		0
1270	CCIGITITICIACAAACICGIICCIGAICCIGIGAAG 13	9
1306	HisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCys 51	0 9
511	GlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCys 53	0

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1506 1578 1735 GGTTCT------TGGAATTTATCAGAC 1755 1366 AATAAAACATAAAATCCTGTTCGGAGTGTTTAACAGCCACAGACCCTCACTGCGGTTGGTGC 1425 1639 ------CAGAATAAAAGTCAG 1653 ||| -----CCAACCAGAGCAACCTACAAAGATGTTTCAGTTGTCAACGTGATGTTCTCCTTC 1734 650 730 ProGlnSerGlyGlnArgGlyTyrGluCysileLeuAsnileGlnGlySerGluGlnArg 749 750 ValProAlaLeuArgPheAsnSerSerSerValGlnCysGlnAsnThrSerTyrSerTyr 769 HisPheAsnIleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMet 807 ArgGluSerCysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGln 827 GlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGlu 847 867 690 PheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeuLeuArgValAspLys 709 710 IleLeuValProValGluValIleLysProIleThrLeuLysAlaLysAsnLeuProGln 729 770 GluGlyMetGluIleAsnAsnLeuProValGluLeuThrValValTrpAsn-----Gly 787 611 GlnCysTyrSerProAlaAlaLysGluValProArgileIleThrGluAsnGlyAspHis 630 651 PheValPheTyrAsnCysSerValHisAsnSerCysLeu---SerCysValGluSerPro 669 670 TyrArgCysHisTrpCysLysTyrArgHisValCysThrHisAspProLysThrCysSer 689 GlyProArgGluGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPhe 848 LeuSerGlyAlaLysSerLysCysThrAsnProArgIleThrGluIleIleProValThr 1654 CCCAACCGG------ACCTGCACCTGTAGCATC------9051 -----CAGATAATTCGAAGCAGTAAAGAAAAACACTACAGTGACTATGGTGGGAAGC ValLeuHisAsnThrCysThrArgLysGluArgCysGluArgSerLysGluProArgArg 1426 CATTCGCTACAAAGGTGCACTTTTCAAGGAGATTGT---------551 PheAlaSerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIleSerVal 571 SerGlnTyrAsnValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaGly 591 ValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 631 HisValValGlnLeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSer |||||||:::||| -------GCAAAAAGTGCCCTAAAATT--------831 AGTGCAAGAAGGTGT------531 1528 1627 1638 1681 808 1483 1507 1462

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1861	GCT
888	ArgAspileAlaSerHisValLysValAlaGlyValGluCysSerProLeuValAspGly 907
1864	111 1875
906	TyrlleProAlaGluGlnIleValCysGluMetGlyGluAla 921
1876	GATTATGAGAGAAACCAGGAACAGTGTCCAGTGGCTGTCGAGAAGACATCAGGAGGAGGA 1935
922	LysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPhe 941
1936	4GGAGAA(
942	PheMetThrLeuThrLeuSerAspLeuLysPro 96
1963	
962	o.
2008	CAACGTGATAGT
982	GlySerAsnvalvalvalMetPheGlyLysGlnProCys994 ::::::::::
2068	GCATCGAACATCACAATGATCCTGAAAGGAACCAGTACCTGTGATAAGGATGTGATACAG 2127
995	LeuPheHisArgArgSerProSerTyrIleValCysAsnThrThrSerSerAspGluVal 1014 :::
1015	LeuGluMetLysValSerValGlnValAspArgAlaLys1leHisGlnAspLeuVal 1033
2185	
1034	PheGlnTyrValGluAspProThrIleValArglleGluBroGluTrpSerIleValSer 1053
2242	TTATCCTACATTGCTCTGCCACATTGTTCCCTTATATTTCCTGCTACCACCTGGATCAGT 2301
1054	GlyAsnThrProilealaValTrpGlyThrHisLeuAspLeuileGlnAsnProGlnile 1073
1074	aThrGlu 109
2356	ATCATTICACATGAATTAAAAGGAAACATAAATGTCTCTGAATATTGTGTGGCGACTTAC 2415
1094	MetThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGlu 1113
2416	TGCGGGTTTTTAGCCCCCAGTTTA2439
1114	ArgProGluGluPheGlyPheIleLeuAspAsnValGlnSerLeuLeuIeLeuAsnLys 1133
2440	AAGAGTICAAAAGIGCGCACGAAIGTCACTGTGAAGCTGAGAGTACAAGAC 2490
1134	114
2491	ACCTACTIGGATIGIGGAACCCIGCAGIAICGGGAGGACCCCCAGAIICACGGGGIAICGG 2550
1149	ProserGlyIleLeuGluLeuLy8FroGlyThrProllelleLeuLy8GlyLy8AsnLeu 1168
2551	GTGGAATCCGAGGTGGACACAGGAAGTGAAATTCAA 2592
1169	uLys 118
2593	262
1189	120
2626	9
1206	Leuile 1207
2686	::: ATTACTAGAAATCAAGATCTTACCACCATCCTTTGCAAAATTAAAGGCATCAAGACTGCA 2745

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1227 2799 2799 124 126 129 129 129	130 132 132 306 133 133 135 135	32 4 6 4 6	3461 1449 352 1151 1151 1153 370 370 370
	GluSerArgValAlaleuGluCy8LysGluAlaPheAlaGluLeuGlnThrAspIleHis		MetLeuThrAsnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGlu
1208 2746 1223 2800 1242 2851 1262	1282 2953 1302 1302 1321 1339 3124	35,177	143° 346° 145° 352° 352° 151° 151° 153° 370° 370°

ζ	1551	MetaspieugluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570
Db	3766	:::
δ	1571	ThrThrLysIleGluAsnAspTrpLysArgLeuAsnThrLeuAlaHisTyrGlnValPro 1590
qq	3826	rccorgaricticadaarggaarcaccaagctaaacaccarrggccactatatgagararca 3885
λŏ	1591	ValSerLysG
qa	3886	AATGGATCCACTATAAAAGTC 3906
ò	1611	Alase
qa	3907	TITAAGAAGAIAGCAAATITIACTICAGAT 3936
ò	1631	ProAspSerLeuArgSerArgThrProMetlleThrProAspLeuGluSerGlyValLys 1650
qq	3937	GIGGAGTACTCGGATGACCACTGCCATTTTGATTTTACCAGATTCGGAAGCA 3987
ò	1651	GlyAspGlnLysGluGl
QC	3988	TTCCAAGATGTGCAAGGAAAGAGACAT
à	1671	LysMetValSerGluIleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeu 1688
OP	4024	CACAAGTICAAAGTAAAAAGTATCTATCTAACAAAGCTGCTGTCGACCAAGGTGGCAATT 4083
ò	1689	Arg
qq	4084	CATTCTGTGCTTGAAAACTTTTTTGAAGCATTTGGAGTTTACCCAACAGCAGA 4137
ò	1709	LeuProLeuAlalleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGly 1728
Ωp	4138	GCTCCATTIGCTATAAAATACTTTTTTTTTTTTTTTTTTT
ờ	1729	IleHisAspProHisValArgHisThrTrpLysSerAsnCysLeuDroLeuArgPheTrp 1748
qq	4198	ATCACAGATCCTGACGTACATATTTGGAAAACAAACAGCCTTCCTCTTCGCTTCTGG 4257
ò	1749	ValasnMetIleLysasnProGlnPheValPheAspIleHisLysAsnSerIleThrAsp 1768
qq	4258	GTAAACATCCTGAAGAACCCTCAGTTTGTCTTTGACATTAAGAAGACACCACATATAGACA 4317
ò	1769	00
qq	4318	Gecigitifetchafdaridecchaeccaficaredatecarricicrecaedaecaa 4377
ò	1789	LeuGlyLysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLys 1808
qq	4378	CTAGGGAAGGAAGCACCAACTAATAAGCTTCTTATGCCAAGGATATCCCAACCTACAAA 4437
δ	1809	AsnTrpValGluArgTyrTyrSerAspIleGlyLyBMetProAlalleSerAspGlnAsp 1828
Ωp	4438	GAAGAAGTAAAAATCTTATTACAAAGCAATCAGGGATTTGCCTCCATTGTCATCCTCAGAA 4497
δ	1829	MetasnalaTyrLeualaGluGlnSerargMetHisMetasnGluPheAsnThrMetSer 1848
q	4498	AIGGAAGAATTITIAACTCAGGAATCTAAGAAACATGAAATTTAATGAAGAAGTG 4557
È	1849	AlaLeuSerGluIlePheSerTyrValGlyLysTyrSerGluGluIleLeuGlyProLeu 1868
QQ	4558	GCCTTGACAGAAATTTACAAATACATGGTAAAATATTTGATGAGATTCTAAATAAA
δ	1869	88
QQ	4618	GAAAGAGAACGAGGGCTGGAAGAGCTCAGAAACAACTCTTGCATGTAAAAGTC 4671

RESULT 8
US-09-023-655-603
Sequence 603, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:

```
RESULT 9
US-08-306-691B-22
i Sequence 22, Application US/08306691B
i Patent No. 5734039
i GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Galabretta, Bruno
APPLICANT: Galabretta, Bruno
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
COORESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gooda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
ITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIF: 19102
COMPUTER: IEM PS/2
COMPUTER: SASTEM: MS-DOS
SOFTWARE: Worderfect 5.1
CURRENT APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2235 CCGCAGATCATGGCCGCGCTGGAGGCCAACCCCACGGAGGACAGAACTGCAGCAC 2294
                              1875 AGCCTTCCTCCGGTTCTGGGTGAACATCCTGAAGAACCCCCCAGTTTGTCTTTGACATC 1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1862 GluGluIJeLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLysLeuAlaTyr 1881
                                                                                                                                                                                                                                                                                                                                                                                                              ATC-----CGTGAAGACAAGCCCCCACTGGCTGTCAANNACTTTTTGAACTTCCTGGAN
                                                                                                                                                                                                                 1722 GluginalaAspiysHisGlyIleHisAspProHisValArgHisThrTrpLy8SerAsn
                                                                                                                                                                                                                                                        1742 CysleuProleuArgPheTrpValAsnMetIleLysAsnProGlnPheValPheAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1842 AsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSerTyrValGlyLysTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1702 ThralaHisArgGlySerAlaLeuProLeuAlaileLysTyrMetPheAspPheLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysSerThrSerGluHisArgLeuGlyLysAspSerProSerAsnLysLeuLeuTyrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysAspileProSerTyrLysAsnTrpValGluArgTyrTyrSerAspileGlyLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2055 AAGGAGATTCCTGAGTACCGGAAGATCGTGCAGGGCTACTACAAGCAGATCCAGGACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2295 AAGTTTGAGCAGGTGGTGGCTTTGATG 2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1882 LysLeuGluGlnValIleThrLeuMet 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1646 GluSerGlyValLysMetTrpHisLeuVal---LysAsnHisGluHisGlyAspGlnLys 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1465 ITTICITIGATIGIAAAATAITITITACITITIAGICTICIAAITIAATAAAGAICCA 1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SerLeuArgSerArgThrProMetIleThrProAgpLeu 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1420 AGAACGTGCGCTTCTGATTAT------TTTACTGGGGTCCATTGTCCAGAT
                                                                                 GENE
                                                                                 BLOOD CELL
                                                                                 O.F
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/09/023,655
FILING DATE: HERBWITH
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: PA-0001 US
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION NUMBER: PA-0001 US
TELECOMUNICATION NUMBER: PA-00
                                                                                 FOR THE DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-964-956-13 (1-1896) x US-09-023-655-603 (1-3458)
APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DET
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
TUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: ALLO ALTO
STREET: CALIFORNIA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3458 base pairs
TYPE: nucleic acid
STRANDEDNES: single
TOPOLOCY: linear
MMEDIATE SOURCE:
LIBRARY: THYMNON4
CLONE: 3191066
US-09-023-655-603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.59e-60
657.00
61.17%
47.25%
6.58%
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Pred. No.:
Score:
Fercent Similarity:
Best Local Similarity:
Query Match:
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1344 1322 1359 1380 269 ර් සි ර් 셤 ò 8 B g 8 6 8 6 8 6 248 212 485 GlnGlyileCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHis 154 ------161 166 701 GlySerValPheGlyValIleValSer------TyrSerAsnLeuAsp 180 197 |||...: | | ||...: 762 GACCGGIICAICAACTICITIGIAGGCAAIACCAIAAAIICI-----ICITAIIICCCA 815 869 MetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAsp 232 268 ThrPheThrIleIleProAspPhe-----AspIleTyrTyrValTyrGlyPhe 101 ValGinThrCysAsnGluProLeuThrThrThr------AsnAsnValAsn AspLys------LeuPhelleAlaThrAlaValAspGlyLysProGluTyrPhePro ------ThrileSerSerArgLysLeuThrLysAsnSerGluAlaAspGly |||||| | GATCATCCATTGCATTCGATGAGAAGGCTAAAGGAAACGAAA-----GATGGT SerSerGlyAenPheValTyrPheLeuThrLeuGlnProGluMetValSerProProGly 4626 282 204 409 475 59 Length:
Matches:
Conservative:
Mismatches:
Gaps: US-09-964-956-13 (1-1896) x US-08-306-691B-22 (1-4626) LysLysGluHisTyrLeuSerGlyValAsn-----FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.,

REGISTRATION NUMBER: 30,480

REFERENCE/COCKET NUMBER: 8321-8

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-8383

TELEFAX: No. 57340396

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 4626 base pairs

TYPE: mucleic acid

STANDEDENESS: double

STANDEDENESS: double

US-08-306-6918-22 2.86e-57 629.50 35.47% 20.58% 6.30% Score:
Percent Similarity:
3
Best Local Similarity:
Query Match:
1 Alignment Scores: Pred. No.: 435 167 702 816 155 642 233 81 486 135 181 198 900 ò g

------CACTGC-----TTTAATAGGACACTTCTGAGAAT 1409 439 996 ---ACTCTAGATGCTCAGACTTTTCACACAGAATAATCAGGTTCTGTTCCATAAACTT 1052 577 LeuVal-----LeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594 360 LeulysGlnIleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGly 379 380 ThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThr 399 440 TyriygaanHisSerLeualaPheValGlyThrLysSerGlyLysLeuLysLysIleArg 459 480 ProvalleuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499 500 ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519 520 LeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThrCysThrArgLys 539 595 PheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSer 614 460 ValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValValAspProGly 479 557 GlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeu 576 540 GluArg---CysGluArgSerLysGluProArgArg-----PheAlaSerGluMetLys 420 ArgGlyIleProValPheThrGluAspArgAspArgMetThrSerValIleAlaTyrVal 400 IleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetVal SerThrIvsGluGlnValTyrThrSerIvsLeuValArgLeuCysLysGluAspThr .322 |||::: ::||| |S06 CTCTIAACAICTATATCCACCTICAITAAAGGAGCCTC-----| | | | | | : : : 1323 -----

28 10:28:28 2004

	1932 194011400000000000000000000000000000000
635	LeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyr 654
1652	1652
9 1	snCysSerValHisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTrp 674
675	CvsLvsTvrArdHisValCvsThrHisAsDProLvsThrCvsSerPhedlnGluGlubra 694
1658	16
695	ValLysLeuProGluAspCysProGlnLeuLeuArgValAspLysIleLeuValProVal 714
1658	1658
715	LysAlaLysAsnLeuProGlnProGlnSe
1659	
1689	ArgGiyTyrGiuCySileLeuasnileGinGiySerGiuGinArgValProAlaLeuArg 754 AATGGCTAAAAATATATTATATATATATATATATATATAT
755	lnAsnThrSerTyrSerTyrGluGlyMetGluIle 774
1713	:::
775	AsnAsnLeuProValGluLeuThrValValTrpAsnGlyHisPheAsn 790
1725	ACGAAGATCCCATTG1763
791	IleAspAsnProAlaGlnAsnLysValHisLeuTyrLysCysGlyAlaMetArgGluSer 810
1764	CAGICC 1769
811	CysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGly 830
1770	recagnoardecricioneccoaccininginaerdrescrightecacGac 1823
831	GlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGly 850
1824	AAATGTGTGCGATCGGAGGAATGCCTGAGCGGG 1856
851	AlaLysSerLysCysThrAsnProArglleThrGluIleIleProValThrGly 868
ה מ ה מ	ACATOGRAFI CHARCAGAL CIGILCI GCCIGCAAI CIANGGAI II II CCCAAAI AGIGGA 1913 BYOBYAGII GII VOI VARAT VAXO I TAYTI BAYAGII VOI VAANI BUGII VA BUGII UDAAAYA GOO
1914	CCCTTGAAGGAGGACAAAGCTGACCATATGTGGCACTGGGACTTTGGATTTCGG 1967
889	AsplleAlaSerHisValLysValAlaGlyValGluCysSerFro 903
1968	AGGAATAATAAATTTGATTTAAAGAAAACTAGAGTTCTCCTTGGAAATGAGAGCTGCACC 2027
904	LeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGlyGluAlaLysPro 923
2028	THEACTITAAGIGAGGACACGAIGAATACAITGAAAIGCACAGITGGICCT 2078
924	SerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPheMetAla 943
2079	GCCATGAATAAGCATTTCAATATGTCCATAATTATTTCAAATGGCCACGGGACAACA 2135
944	ArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArg 963
2136	

2549 2930 1065 AspLeulleGlnAsnProGln-----IleArgAlaLysHisGlyGlyLysGluHisIle 1083 AsnIleCysGluValLeuAsnAlaThrGlu---MetThrCysGlnAlaProAlaLeuAla 1102 2717 LeulysGlyLysAsnLeulleproProValAlaGlyGlyAsnyalLysLeuAsnTyrThr 1182 GluSerProAsn---LeulleGlyArgHisLysValMetAlaArgValGlyGlyMetGlu 1220 TyrserPro-------GlyMetValTyrIleAlaProAspSerPro 1233 ::: ::: ::: ::: ::: |||||||||||| || TTCACAGATTGTTATTACTACTTGGG 3098 PhelleValAlaValLeulleAlaTyrLysArgLysSerArgGluSerAspLeuThrLeu 1271 LysArgLeuGlnMetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGlu 1291 AlaPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGly 1311 ValPheGluAlaPheGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIle AspAsnValGlnSerLeuLeulleLeuAsnLysThrAsnPheThrTyrTyrProAsnPro ValLeuValGlyGluLysProCys---ThrValThrValSerAspValGlnLeuLeuCys LeuSer-----LeuProAlalleValSerileAlaValAlaGlyGlyLeuLeuIleIle TACGATGCAAGAGTACACACTCCTCATTTGGATAGGCTTGTAAGTGCCCGGAAGTGTAAGC ::: TCTAGACACATTTCAATTGGTGGAAAAACATGTACTTTAAAAAGTGTGTCAAACAGTATT -------SerGlyAsnThrProlleAlaValTrpGlyThrHisLeu GlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySer GGTCCTATGGCTGGTGGCACTTTACTTACTTTAACTGGAAATTACCTAAACAGTGGAAAT AsnvalvalvalMetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyr ::: ||| ||| :::::::

CITGAAIGTIATACCCCAGCCCAACCAITICAACIGAGTIIGCIGTIAAAIIGAAAAIT AspArgAlaLysIleHisGlnAspLeuValPheGlnTyrValGluAspProThrIleVal LeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeu IleValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnVal 1044 ArgileGluProGluTrpSerIleVal----2490 1084 2610 2826 2979 3039 2550 1103 2667 1123 2718 1143 2766 1163 1183 2871 1202 2931 1221 1234 1252 2253 2313 1066 2193 984 1004 1024 2373 964 1053

	546 ATGGCT	135 GlnGl	606 AGAĞĞ	155 LYSLYS		702 AGCCAC		:: 762 GACCG	198	816 GATCA	213 MetPh	870 TT	233 ThrPh	006	249 SerSe	954 GAAAG	269 SerTh	996AC	289 AlaPh	1053 GGATT	302 ArgSe	1113 AGAT	320 Alava	1173 GCCCA	340 SerLy	1233 GCAC	360 Leul	1293 ATCA	380 ThrLe	1322	400 IleAs	1322	420 ArgG]	1323	
è	qq	8	q	ò	Q	Š ₽	8 8	· 요	ò	셤	ð	qq	ζŏ	qg —	ò	qa	ò	qq	ò	අ ධ	λο	Db	ò	qu	λŏ	qa	ò	qq	δ	업	ò	qu	δ	qa	_
:: ::::: Db 3219 CCAACTACAGAAATGGTTTCAAAT	Qy 1312 IleProPheLeuAspTyrArgThrTyrThrMetArgValLeuPheProGly1leGluAsp 1331	DD 3243GAATCTGTAGACTACCGAGCTACTTTTCCAGAAGATCAGTTTCCTAATTCATCTCAG 3299	Qy 1332 HisProValLeuArgAspLeuGluValPro 1341	Db 3300 AACGGTTCATGCCGACAAGTGCAGTATCCT 3329	RESULT 10 PCT-US93-06251-27	Applicatio RMATION:	; APPLICANT: WICKSETOM, EIIC and KILE, Jason F.; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates		ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER; STREET: 400 Garden City Plaza	; CITY: Garden City ; STATE: NY		; COMPUTER READABLE FORM; MEDIUM TYPE: Floppy disk	COMPUTER: IBM PC compatible) OPERATING SYSTEM: PC-DOS/MS-DOS	ATA:	; APPLICATION NUMBER: PCT/US93/06251 ; FILING DATE: 19930630	; CLASSIFICATION: ; ATTORNEY/AGENT INFORMATION:	; NAME: DIGIGILO, Frank S. ; REGISTRATION NUMBER: 31,346	DOCKET NUMB ATION INFOR	റം	; INFORMATION FOR SEQ ID NO: 27:	; SEQUENCE CHARACTERISTICS: ; LENGTH: 4626 base pairs	ES 2	; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic)	PCT-US93-06251-27	<pre>nent Scores: 2.86e-57</pre>	Score: 629.50 Matches: 282 Percent Similarity: 35.47% Conservative: 204	6.30% Mismacches:	Gaps:	-09-964-956-13 (1-1896) x PCT-US93-06251-27 (1-4626)	62 HislleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal	375 CACATTTTCCTTGGTGCCACTAACTACATTTATGTTTTAAATGAGGAAGACCTTCAGAAG	81 LeuValThrHisGluThrGlyProAspGluAspAsnProLysCysTyrProProArg11e :::		101 ValGlnThrCysAsnGluProLeuThrThrThr	Db 486 TGTCAGGACTGCAGCAGAAAGCCAATTTATCAGGAGGTGTTTGGAAAGATAACATCAAC 545

116	6 LysMetLeuLeuleAspTyrLysGluAsnargLeulleAlaCysGlySerLeuTyr 134
139	5 GlnGlylleCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGluProTyrHis 154
15.	HisTyrLeuSerGlyValAsn
	GlyservalPheGlyValIleValSerTyrSer
18	1 AsplysLeuphellealaThralaValAspGlyLy. 2 GACCGGTTCATCAACTTCTTTGTAGGCAATACCATAAATTCT
19	8ThrileSerSerArgLysLeuThrLysAsnSerCerserArgLysLeuThrLysAsnSerCerserCearTcGArArCAGTGAGAAGGAAAGGAAA.
21.	3 MetPheAlaTyrValPheHi :::::: 0TTTATGTTTTTGACGGA
90 33 90 33	3 ThrPheThrllelleProAspPhe ::::: ::: 0GATGTTTTACCTGAGTTCAC
2 2 4 5	9 SerSerGly 4 GAAAGCAAC
9 6	9 SerthrihrlysgluglnValTyrThrSerLysLeuValArgLeuCy
101	aPheabnSerTyrValGluValProlleGlyCys
30	02 ArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGly 319
33	hrLeuglyval ::: paataggagco
3,	rLysGlyGlnLysArgLysMetLysS :::: acaaagcaagccagaTTCTGCCGAAC
w 0	O LeulysGlnIleAsnAspArgIleLysGluArgLeuGlnSerC\\ :::
	0 ThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLeuLeuThr 399
13	
4	eAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyValSerAspMetVal 419
13	13
	20 ArgGlyIleProvalPheT
13	23AICGIC 132

ДP			
δλ	460 ValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValValAspProGly 479	δí	
qq	1344AGATGTCTCCAGCAT1358	g (
٨	480 ProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499	ð £	831 GlnCysThrLeuArgGlnH: ::: :824 &&aqqqqqqqqqqqqqqqqqqqqqqq
qq	1359 1379 TITIACGGACCCAATCATGAG 1379	3 8	
Qy	500 ArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519	Ŝ	
qq	1379	3 8	
0y	520 LeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThrCysThrArgLys 539	Š	869 FIOAIGGIUGIYGIYINIL
qq	1380	9 8	1914 (11) CARGARAGA CARACA CAR
δý	540 GluargCysgluargSerLysGluProArgArgPheAlaSerGluMetLys 556	Š 1	
qo	1410 TCATCAGGCTGTGAAGCGCGCGGGGGTGAATATCGAACAGATTTACCACAGGTTTGCAG 1469	ad é	
ò	557 GlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGlnTyrAsnValLeu 576	ਤੋਂ ਹ	904 LeuvalAspGlyTyrileP:
DÞ	1470	g ;	2028 TTGACTTTAAGTGAGAGCAG
ζ	577 LeuValLeuGluThrTyrAsnValProGluLeuSerAlaGlyValAsnCysThr 594	Š €	
qq	1506 CICTTABCATCTATATCCACCTTCATTABAGGAGACTCACC 1547	3 8	2019 GCCAIGANIAAGCAIIIC
ò	595 PheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIleGlnCysTyrSer 614	දු දු	944 AIGSEISEIGIILEUIYII
Ор	1548 ATAGCTAATCTTGGGACATCAGAGGTCGCTTCATGCAGGTTGTGGTTTCTCGATCAGGA 1607	i è	
ò	615 ProAlaAlaLysGluValProArgllelleThrGluAsnGlyAspHisHisValValGln 634	ờ €	
QQ	1608 ccarcaacccarardaaarrrrcacagaacrcccarrcaarg 1652	1 8	
ò	635 LeuGlnLeuLysSerLysGluThrGlyMetThrPheAlaSerThrSerPheValPheTyr 654	; E	
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ò	655 AsnCysSerValHisAsnSerCysLeuSerCysValGluSerProTyrArgCysHisTrp 674	2 E	::: ::: : : : : : : : : : :
q	1653	3 8	
λõ	675 CysLysTyrArgHisValCysThrHisAspProLysThrCysSerPheGlnGluGlyArg 694	; ; ;	
qq	1658 1658	3 8	
λö	695 ValLysLeuProGluAspCysProGlnLeuLeuArgValAspLysIleLeuValProVal 714	;	
ф	1658 1658	3 8	
۵,	715 GluValIleLysProlleThrLeuLysAlaLysAsnLeuProGlnProGlnSerGlyGln 734	Š 1	
qa	1659 GAAGTGATGTGGAGCATACATTAAACCAA 1688	9 <i>(</i>	
δλ	735 ArgGlyTyrGluCysIleLeuAsnIleGlnGlySerGluGlnArgValProAlaLeuArg 754	È ·	1066 ASPLEULIEGIDASDETOG
ΩÞ	 1689 AATGGCTACACTGGTTATCACT	යු ්	
δ	a) -	8	1084 AsnIleCysGluValLeuA ::
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ò		à	LeuGl
qa	 1725 ACGAAGATCCCATTG1763	අු	
ر م	791 IleAspAsnProAlaGlnAsnLysValHisLevTyrLysCysGlyAlaMetArgGluSer 810	λο 	1123 AspAsnValGinSerLeuL

1764	::: CAGTCC 1769
811 1770	CysGlyLeuCysLeuLysAlaAspProAspPheAlaCysGlyTrpCysGlnGlyProGly 830
831	GlnCysThrLeuArgGlnHisCysProAlaGlnGluSerGlnTrpLeuGluLeuSerGly 850 :::
851 1857	AlaLysSerLysCysThrAsnProArglleThrGlulleIleProValThrGly 868 :::::
869	ProArgGluGlyGlyThrLysValThrIleArgGlyGluAsnLeuGlyLeuGluPheArg 888
889 1968	
904 2028	LeuValAspGlyTyrIleProAlaGluGlnIleValCysGluMetGlyGluAlaLysPro 923
924	SerGinHisAlaGlyPheValGluIleCysValAlaValCysArgProGluPheMetAla 943 ::: ::
944	ArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArg 963 :::
964	GlyProwetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySer 983
984	AsnvalvalvalmetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyr 1003 :::
1004	IleValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnVal 1023 ::: :::::::: CTTGAATGTTATACCCCAGCCCAACCATTTCAACTGAGTTTGCTGTTAAATTGAAAATT 2372
1024	ABPAYGAlaLySIleHisGlnAspLeuValPheGlnTyrValGluAspProThrIleVal 1043
1044	ArgileGluproGluTrpSerileVal1052
1053	SerGlyAsnThrProlleAlaValTrpGlyThrHisLeu 1065 AGTTTTCTATTTTGCTTTGCCAGTGGTGGGAGCACAATAACAGGTGTTGGGAAAAACCTG 2549
1066 2550	
1084	AsnIleCysGluValLeuAsnAlaThrGluMetThrCysGlnAlaProAlaLeuAla 1102
1103	LeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIleLeu 1122
1123	AspAsnValGlnSerLeuLeulleLeuAsnLysThrAsnPheThrTyrTyrProAsnPro 1142

CT 2765	le 1162 AA 2825	hr 1182 2870	ys 1201 	ilu 1220 	ro 1233 AT 3038	:le 1251 3GG 3098	.eu 1271 .GC 3158	ilu 1291 GC 3218	ily 1311 3242	NSD 1331 PAG 3299		ods of
GATCTCATTTATGTACATAATC	ValPheGlualaPheGlyProSerGlyIleLeuGluLeuLysProGlyThrProIleIle :: GTGTTTAAGCCTTTTGAAAAGCCAGTGATGATCTCAATGGGCAATGAAAATGTACTGGAA	8G1YLysAsnLeulleProProValAlaGlyGlyAsnValLysLeuAsnTyrThr ::::: GGGAAATGATATTGACCCTGAAGCAGTTAAAGGTGAAGTG	ValleuValGlyGluLysProCysThrValThrValSerAspValGlnLeuLeuCy :::	eulleGlyArgHisLysValMetAlaArgValGlyGlyMetGlu ::: rGCTGAAATTGAACAGCGAGCTAAATATAGAG	YTSerPro	LeuSerLeuProAlaileValSerileAlaValAlaGlyGlyLeuLeuIleile :::	elleValAlaValLeulleAlaTyrLysArgLysSerArgGluSerAspLeuThrLeu 	LysargleuGlnMetGlnMetaspasnLeuGluSerargValalaLeuGluCysLysGlu 	aPheAlaGluLeuGlnThrAspIleHisGluLeuThrSerAspLeuAspGlyAlaGly ::: ::::: AACTACAGAAATGGTTTCAAAT	eProPheLeuAspTyrArgThrTyrThrMetArgValLeuPheProGlyIleGluAsp ::: -GAATCTGTAGACTACCGAGCTACTTTCCAGAAGATCAGTTTCCTAATTCATCTAG	ValPro 1341 TATCT 3329	BA exity Nucleic Acid Targets and Method 300,958A 331 070 624
GATGGGATCCTTTCCAAATACTTT	ValPheGlualaPheGlyProSerGlyll ::: GrGTTTAAGCCTTTTGAAAAGCCAGTGAT	LeuLysGlyLysAsnLeuIleProProValAlaGlyGlyAsnVal -:: ATTAAGGGAAATGATTTGACCTGAAGCAGTTAAAGGTGAAGTG	ValleuvalGlyGluLysProCys:::	GluSerProAsnLeulleGlyArgHisLysValMet;	Tyrserpro	LeuSerLeuProAlalle ::: TTCACAGGATTGATTGCTGGTGTT	PheileValAlaValLeuileAla 	LysArgleuGlnMetGlnMetAsp :::::: TACGATGCAAGAGTACACACTCCT	AlaPheAlaGluLeuGlnThrAsp ::: CCAACTACAGAAATGGTTTCAAAT	IleProPheLeuAspTyrArgThi ::: GAATCTGTAGACTACCGAGCT	HisProValLeuArgAspLeuGluValPro	Application US/0930095 495319 MRATION: MCGLGland, Michael MCGLGland, Michael MCGLGLAND: MCBNION: Reduced Compl VENTION: 1998-04-27 CCATION NUMBER: 60/098, CCATION NUMBER: 60/18,
Db 2718	Oy 1143 Db 2766	Oy 1163 Db 2826	Oy 1183 Db 2871	Oy 1202 Db 2931	Qy 1221 Db 2979	Oy 1234 Db 3039	Qy 1252 Db 3099	Qy 1272 Db 3159	Oy 1292 Db 3219	Oy 1312 Db 3243	Oy 1332 Db 3300	RESULT 11 US-09-300-958A-24 Sequence 24, Ap. Patent No. 6495 GENERAL INFORMA APPLICANT: Mc APPLICANT: Tr TITLE OF INVENT FILE REFERENCE CURRENT APPLICAT PRIOR FILING DEPRIOR APPLICAT PRIOR FILING DEPRIOR APPLICAT PRIOR FILING DEPRIOR APPLICAT PRIOR FILING DEPRIOR FILING DEPRIOR APPLICAT PRIOR FILING DEPRIOR FILING DEPRIOR APPLICAT PRIOR APPLICAT TYPES DAM TYPE
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	Alignment Sc Pred. No.: Score: Percent Simi Best Local & Query Match. DB:	or Ting	es: rity: ilarity:	3.22e-24 323.00 36.19% 3.35% 3.23%	Length: Matches: Conservative: Mismatches: Indels:	2433 128 128 241 42	
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	۲۵	56	ValAspGlu	ArgThrGlyHisI	ValAspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLySL	AsnArgIleTyrLysLeuSer	75
	QQ	61 (CTGAGCCAC	: SGATGGAAAGACGC	: : :	TTAA	120
	ò	76	SerAsple	euLysValLeuValThrHi	hrHisGlu	ThrGlyProAspGlu	06
	Db	121	AGCAACCTO	::: GCAACCTCAGCTTCTTGCCAGGCGGGGAGTA	GCGGGGAGTACCAAGAG	CCAAGAGCTACTGTGGAGTGCAGATGCT	180
	È	91	AspAsnPro	spasnProLysCysTyrProProArgI	leval	CysAsnGlu	106
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	٥٨	107	ProLeuTh:	rThrThrAsnAsnV	roLeuThrThrAsnAsnValAsnLysMetLeuLeull	4;	126
	qq	217 (ccaaagcg	rgactgtcaaaact.	-ย	ccactcaacagcagccac	273
	ά	127	_	aCysGlySerL	-SerLeuTyrGlnGlyIleCys	/sLysLeuLeuArgLeuGluAsp	145
	qa	274	CTGCTCAC	ccrdrddcacaacaa	ccrrcagcccccrgrdr	cacceccricaeccccrististerracaricacaraceaec	333
	δ	146	LeuPheLy:	sLeuGlyGluProTyrHi	sLysLysGluHi	sTyrLeuSerGlyValAsnGlu	165
	qa	334	TTTAC	CTTTAGCCCAA		GATGAG	354
	à	166	erGly	erValPheGlyValil	eValSerTyrSerAsn	LeuAsp	180
	Пр	355 (GCCGGTAAT	AATGTCATT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CTGGAGGATGGCAAGGGTCAT	390
	λ̈	181		-AsplysleuPhel	laThrAl	aValAspGlyLysProGluTyr	195
	qq	391	TGTCCCTT	CTTTGACCCCAACTTCAAGT	CCACGGC	GTTGATGGTGAGCTG	444
	ò	196	Phe		Pro	oThrlleSerSerArgLysLeu	204
- 1	qq	445	TACACTGG	AACAGTCAGTAGCT	TCCAGGGAAACGACCCA	TACACTGGAACAGTCAGTAGCTTCCAGGGAAACGACCACCAGCCATTTCCCGGAGCCAGAGT	504
	ò	205		nSerGluAlaAspG	aAspGlyMetPheAlaTyrVal	aTyrvalPheHisAspGluPheValAla	1 224
	qq	505	TCCCGCCC	CACCAAGACTGAGA	GCTCCCTCAACTGGCTA	cogececaccaagaergagagerecercaacrageracaagaecergeerridragee	564
	ò	225	SerMet116	IleLysIleProSerA 	eraspīhrPheīhrileile 	eProAspPheAspIleTyrTyr	~
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	ò	245	ValTyrGly	TyrGlyPheSerSerGlyAsnPheVal	snPheValTyrPheLeu	TyrPheLeuThrLeuGlnProGluMetVal	264
	QD	625	TTCTTCAG	cgagaccagg	CTTCAGCGAGACGGGCCAGGAGTTTGAGTTCTTT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	. 660
	ò	265	SerProPro	oGlySerThrThrL	roGlySerThrThrLysGluGlnValTyrThrS	erLysLeuVa	284
	qq	661			GAGAACACCATCGTGTCCCGAGTTGC	CCGAGT	969
	È	285	LysGluAsj	pThrAla		LysGluAspThrAla	296
	q	697	AAGGGCGA	i igagggtggagagg	gggrgtrgcagcaacgc	regaccretritereaager	756
	ò	297	Prollegi	yCysGluArg	SerGlyValGluTyr	ProlleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyr	314
_	අු	757	CAGCTCCT	gridercedidecera	argardddrrrcccrrr	AACGIGCIACAAGAIGICITC	816

10.00			Qy 613TyrSerPro
		LeuSerLysAlaGlyAlaValLeuGlyArg	Db 1837 GCCAGCTACTGCCC
Age of Sec.		8178CCTGAACCCCAACCTTGAGGGTTGGCGC 846	Ov 620ValProArgile
ع _{يد پ} شتند خ		LysGlyGlnLysArgLysMetLysSerLeu	1897 7841
· · · · · · · · · · · · · · · · · · ·		847 AAGACCCTTTCTATCGGGGGTCTTTACCTCCCAGTGGCACAGAGGGACCACAGAA 900	3 5
ist his		GluserAlaLeuCy	979
a Cara		901 GGCTCTGCCATCTGCGTCTTCACCATGAATGATGTGCAGAAGGCCTTT 948	1945
SANC.		372 GlnSerCvsTvrArdGlvGluGlvThrLeuAspLeuAlaTrpLeuLvsAsp 390	Qy 658 IH1SASDSerCysbe
grap who			2005
over er jo			Qy 678 gHisValCysThrHi
ang tumb			Db 2027TTTTGT
		GI GCCCACACGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy 693G
0 - 0		AlaProLeuGlyValSerAsp	Db 2068 AAACTCTTCCTAAAC
744.5		TCGTCCCTGCAGCTCCCAGACCGAGTGCTGAACTTCCTCAAGGATCACTTCTTGATGGAT	Oy 705LeuArgVa
· · · · · · · · · · · · · · · · · · ·			Db 2128 CTACCACCTGAGAC
* e q. e y e		.129 GGGCAGGTCCGCTGCTGCTGCTGCAGCCCAGAGCCCCCCTACCAGCGTGTGGCT 1188	Oy 722 uLysAlaLysAsnL
ing tree!			2188
il te vergy		189 GIGCACCGIGIGCCIGGCCIGCACAGCACTIAIGAIGICCIAÍTÍCIGAGCACIGGIGAI 1248	
t the gra		_	22. 22.
\$977E		.249 GGCGCCTGCACAAAGCAGTGACCCTGAGCTCCAGAGTCCATCATTGAGGAG 1302	745
innýkk u		473 ValGinValValAspProGlyProValLeuArgAspMetAlaPheSerLy8AspHisGlu 492	2308 CGAG
wa godf ^{was}		1303 CTGCAGATCTTCCCTCAAGGACAGCCTGTGCAGAACCTGCTCTTGGACAGCCATGGGGGA 1362	2000 CTIT.T 10
genes a 110/11		ThrArgValProValGluS	077-9
*10*0***		1363 CTGTTGTATGCCTCCTCCCCATTCCGGGGTGGTGCAAGTGCCCGTAGCCAACTGCAGCCTG 1422	; Patent No. 6576441 . CENTEDI INFORMATION.
ere (en ency)			, APPLICANT KIMURA, TOTU e
			FILLE REFERENCE: 0020-4426
· • · · · · · · ·		530ÇyşValLeuHisAsnThr 535	CURRENT AFFICATION 199
· · · · · · · · · · · · · · · · · · ·	,,	- - - - - - - - - - - -	; SOFTWARE: PatentIn versio
entinigi se regel		CysThrArgLysGluArgCys	; SEC ID NO 3 ; LENGTH: 3524 . TYDE: DAM
koning 15	•	1543 ATTGAGGGTGCCAGTGTCAAGGAACTCTGCAAGAATTCCTCATACAAGGCCCGGTTTCTT 1602	ORGANISM: Homo sapiens
034 (7)7)	δλ	553 SerGluMetLysGlnCysValArgLeuThrValHisProAsnAsnIleSerValSerGln 572	, NAME/KEY: 5'UTR . IOCOTION (1) (38)
	. da	1603 GTGCCAGGTAAGCCATGTAAACAAGTCCAAGATCCAAACACAGTGAACACCCTGGCC 1662	OTHER INFORMATION:
. VIV	ζ	573 TyrAsnValLeuLeuLeuValLeuGluThrTyrAsnValProGluLeuSer 588	CCATION: (2706) (3524)
SWS CV:N	 QQ		, CIRER INCOMPILOR: , NAME/KEY: CDS . IOCETION: (39) (2702)
HV Shore ye	δ	589 AlaGlyValAsnCysThrPheGluAspLeuSerGluMetAspGlyLeuValValGlyAsn 608	ORMATI A-3
oratifation	••	1723 GCTTCTGCCTCCTGCCGCGTGTACCCACCGGGAACCTGCTGCTGGTGGAAGC 1776	Alignment Scores:
negawa	٥٨	609 Gln	
yg-pod engl	qa	1777 CAGCAGGGTITGGGGGGTGTTCCAGTGTGGTCGATAGAAGAAGGATTCCAGCAGCTTGTG 1836	Percent Similarity: 36.9 Best Local Similarity: 22.7
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637 ATCTACCGTAGCCTTGGGGACCGG-255 275 290 209 383 437 453 682 661 중음 ò 2 d d d 132 406 TITIGICAAGGIGCICCIGCIICGIGAC----GAAICCACGCICTICGIGIGCGGCICC 459 ---LeuTyrGlnGlyileCysLysLeuLeuArgLeuGluAspLeuPheLysLeuGlyGlu 151 :::::::: TACCTGAGCCACTACCCCGTGTTCGTGGGCAGCGGGCCTGGTCGTCGTCGCCTGCAGAG 201 255 :::|||
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:::||| 357 97 ProProArgIleValGlnThrCys------AsnGluProLeuThrThrAsn 112 405 ------ProTyrHisLysLysGluHisTyrLeuSerGlyVal 163 4 GlyPheAsnHisLeuValValAsp------GluArgThrGlyHisIleTyr 64 78 -----CysLeuLeuSerHisLeuLeuMetValGly 19 ::: ||| ::: 316 CGGTATCAGCGAAGCTTACCTGCGGCGTCCAACCCCAGTGAC--------113 AsnValAsnLysMetLeuLeulleAspTyrLysGluAsnArgLeulleAlaCysGlySer 20 MetGlySerSerThrLeuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSer Lysval-----LeuvalThrHisGluThrGlyProAspGluAspAsnProLysCysTyr ------ArgGlyGluProAlaGlu Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-964-956-13 (1-1896) x US-09-077-940A-1 (1-3692) PheValThrPhe------TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1) ... (18)
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: (19) ... (2682)
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: (2682)
OTHER INFORMATION:
NAME/KEY: 9'UTR
LOCATION: (2683) ... (3653)
OTHER INFORMATION:
NAME/KEY: POLYA site
LOCATION: (3654)... (3692)
OTHER INFORMATION: Score:
Score:
244.50
Percent Similarity:
35.69\$
Best Local Similarity: 22.17\$
Query Match:
2.45\$ Alignment Scores: US-09-077-940A-1 40 142 9 0.5 9 79 358 133 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 à g

TTCTCAGATGGGATGCTCTTCACAGCCACAGTAACTGACTTCCTAGCCATGGACGCTGTT 636 ---TyrserAsnLeuAspAspLysLeuPhelleAlaThrAlaValAspGlyLysProGlu 194

164 AsnGluSerGlySerValPheGlyValIleValSer-----

997 -----ACTCCTAGCAACAGCATCCCTGGCTCTGTGCCTTTGACATGAACCAA 1050 1195 ccrahcaagarrcrcaacrrrgraaagacccaccaccaghagacgaaggagggggccrcc 1254 .255 CTGGGCCACTCGCCTTGGATTGTGAGACTCTGATACGGCACCAGCTGACCCGAGTGGCT 1314 ------ArgValAspGlyProArgGlyAsn 466 363 IleAsnAspArgIleLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeuAsp 382 323 GlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSerLysGly 342 958 -----AGCCTTGGCGGCCGTCCA------996 343 GlnLysArgLysMetLysSerLeuAspGluSerAlaLéuCygIlePhelleLeuLysGln 362 TyrpheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLysGluGln 274 ----GAGTTTAACTATCTGGAAAAG 792 ------GlyProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeu AlaTyrval -----TyrLysAsnHisSerLeuAlaPheValGlyThrLysSer -----PheAsnSerTyrValGluValProIleGlyCysGluArgSerGly---ValTyrThrSerLysLeuValArgLeuCysLysGluAspThrAla------195 TyrPheProThrIleSerSerArgiysLeuThrLysAsnSerGluAlaAspGlyMetPhe 215 AlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThrPhe 235 ThrilelleProAspPheAspIleTyrTyrValTyrGlyPheSerSerGlyAsnPheVal AlaLeuGlnTyrGluThrValGlnValValAspPro-----------CATGAC----TCCAAGTGGTTTAAAGAGCCA---|||||| 745 TACTTCTTCCGGGAGATCGCCATG--------CCCACACTGCGCACAGTAAAG---GlyLysLeuLysLygIle-----467 g ò 8

දු දු 8 8 . & g 8 6 8 8 8 6 6 6 6 6 원 상 명 8 8 8 8 8 6 6 6 6 රි පි ઠે 1495 GCTGGTGAGTGGGGACAACGACTTCTGAGCCTGGAGCTAGATGCTGCCTCAGGTGGCCTG 1554 1555 CTGGCAGCCTTCCCCGCTGTGTGTGTGTTCCTGTTGCCGGCTGCCAGCTGTACTCG 1614 TyrIleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGln 514 482 CAGITGAGGGCAGICAGCITICCIGAAGAIGAIGAACCCCITAATACIGICGACIAICAC 541 56 ValĄsp-------GluArgThrGlyHisIleŢyrLeuGlyAlaValAsnArg 70 71 IleTyrLysLeuSerSerAspLeuLysValLeuValThrHisGluThrGlyProAsp--- 89 20 MetGlySerSerThrLeuLeuThrArgGlnProAlaProLeuSer-----Gln 35 36 LysGlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPheAsnHisLeuVal 55 5 ProTrpAsn-----TrpThrCysLeuLeuSerHisLeuLeuMetValGly 19 515 SerCys---GlyGluCysLeuGlySerGlyAapProHisCysGlyTrp 529 3694 130 101 227 167 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-964-956-13 (1-1896) x US-09-653-274-3 (1-3694) 1.62e-13 228.50 37.02% 20.83% LENGTH: 3694
; TYPE: DNA
 ORGANISM: HOMO Sapiens
; FEATURE:
; NAVE/KEY: CDS
; LOCATION: (434)..(3694)
US-09-653-274-3 Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
2
Query Match:
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AAACTGACATGGCGATCAAGAAAACGGGAAAAACTGTGCTATGAAAGGCAAGCAT 775

101	ValGinThrCygAsnGluProLeuThrThrThrAsnAsnValAsnLysMetLeuLeuIle 120
C)	IyriysGluAsnArgLeulleAlaCysGlySerLeuTyrGlnGlylleCysLys 13
812	CCAAGAAACGATGAGATGGTTTTTTTTTTGTGGTACCAATGCATTCAATCCCATGTGTGAGA 871
140	LeuleuargLeuGluaspLeuPhelysLeuGlyGluProTyrHisLysLysGluHisTyr 159
9 ,	erGlyserValPheGly 17
172	ATTAGTGGCCTGGCGAGATGCCCGTTTGGTGCCGGGCAGACGAGATGTTGCCCTCTTTGCT 9/0 ValT1eValGaTTvTGaTAGATGGTGTGATAGATAGTGATGATGATGATGTTTGTGTGTTTTGTGTTTTGTGTTTGTTG
192	LysProGluTyrPheProThrIleSerSerArgLysLeuThrLysAsnSerGluAlaAsp 211
212	yMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSer 231
232	PheaspileTyrTyrValTyrGlyPheSerSerGly 251
1097	
252	GlnProGluMetValSerProProGlySerThrTi ::: .daaATCGCTGTCGAACATAATATT
272	LysGluGlnValTyrThrSexLysLeuValArgLeuCysLysGluAspThrAla 289 :::
290	
303	SerGly
3 3	SerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeu 335
336	PheThrValPheSerLygGlyGlnLysArgLysMetLygSerLeuAspGluSerAlaLeu 355
356	CysilepheileLeuLysGlnileAsnAspArgileLysGluArg 370
371	
386 1537	LeulysvallysaspileProcysSerSerala-LeuleuThrileAspAspAs 403
403	

OY 30 ProhlaProLeuSerGlnLysGlnArgSerPheValThrPheArgGly 45	Qy 46 GlubroAlaGluGlyPheAsnHisLeuValValAspGluArgThr 60	Oy 61 GlyHisIleTyrLeuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysVal 80	Qy 81 LeuValThrHisGluThrGlyProAsp	Qy 92 AsnProLysCysTyrProProArgIleValGlnThrCysAsnGluProLeuThrThr 110	Oy 111 ThrashashValashLysMetLeuLeuIleAspTyrLysGluAshArgLeuIleAlaCys 130	Qy 131 GlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149	9y 150 GlydluProTyrHisLysCysGluHisTyrLeuSerGlyVal 163	Oy 164AsnGluSerGlySerValPheGlyVallleValSerTyrSerAsnLeuAspAsp 181	Qy 182 LysLeuPhelleAlaThralaValAspGlyLysProGluTyrPheProThrIleSerSer 201	Qy 202 ArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGlu 221 :: :: :: :: 583 GATGCGTTATTATCGAAGCATGGGTGATGGATGGGTCTGCCCTTCGCACAATAAAA 636	Qy 222 PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp 241 ::: ::	Qy 242 IleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPro 261	Qy 262 GluMetValSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuVal 281 :::::::	Oy 282 ArgLeuCysLysGluAspThrAla	Qy 293 TyrValGluValProIleGlyCygGluArgSerGlyVal 305 ::::::::	Qy 306 GluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThr 325	326	943	
Qy 421 ylleProvalPheThrGluAspArgAspArgMetThrSerVal435	Oy 436 -IlehlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGlyLysLe 455	Oy 455 ulyslyslle458 :: Db 1777 ACTTAAAGTTCTGGGAAAGACCAGTCCTTTCTCTTTGAACGACAGCGTATTACTGGAAGA 1836	Qy 459ArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnValVa 476	Qy 476 lAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIl 496 ::: :: Db 1897 CTCATTACAGTTGGATAAAGATCACCACGCTTTATATGT 1935	Qy 496 eMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSerCy 516	Oy 516 sGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsmTh 535	Oy 535 rCysThrArg 538 Db 2053 CTGTGGTAGA 2062	RESULT 15 US-09-653-274-5 ; Sequence 5, Application US/09653274		; AFFLICANT: Mize, Nancy K ; APPLICANT: Mize, Nancy K ; APPLICANT: Tang, Y. Tom ; APPLICANT: Liu, Chenghua	and Maate tides and	; CURRENT APPLICATION NUMBER: US/09/653,274 ; CURRENT FILING DATE: 2000-08-31 ; PRIOR APPLICATION NUMBER: 09/491,404 ; PRIOR FILING DATE: 2000-01-10) NUMBER OF SEQ ID NOS: 13 ; SEQ ID NO 5 : ; LENGTH: 3261		1.45e-13 Length: 228.00 Matches: 37.30% Conservati	DEST LOCAL SIMILATILY: 20.85\$ MISMACCHES: Query Match: 2.28\$ Indels: DB: 4 Gaps:	-09-964-956-13 (1-1896) x US-09-653-274-5 (1-3261)	Oy 10 CysLeuLeuSerHisLeuLeuMetValGlyMetGlySerSerThrLeuLeuThrArgGln	ממ

cagetcaatagcatecetggttetgetgtetgtgtgtgtattagcatggatgacattgaaaa 1014	GINIleAsnAspArgIleLysGluArg	ArgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAspIleProCysSerSer	::: CGAAGACAAAGTGCCAAAGGCCAAGGCTGGCTGTGTGCAAAACACGGCCTTGCCGAAAG 1133	Ala-LeuLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLe 413	TIATAAAACCICCATCGATTTCCCGGATGAAACTCTGTCATTCATCAAATCTCCATCCCT 1193	uGlyValSerAspMetValArgGlyIleProValPheThrGluAspAr 429	1194 GATGGACTTGCCGTTCCACCCATTGCCGATGAGCCCTGGTTCACAAGACTCGGGTCAG 1253	429 gaspargmetThrSerValIlealaTyrValTyrLysAsnHisSerLe 445	:::	uAlaPheValGlyThrLysSerGlyLysLeuLysLyslle	GAAGCTGGCATGGTACTTAAAGTTCTGGCAAAGACCAGTCCTTT 1373		1374 CTCTTTGAACGACGGTATTACTGGAAGAGATTGAAGCCTACAACCATGCAAAGTGCAG 1433	nAlaLeuGlnTyrGluThrValGlnValValAspProGlyProValLeuArgAspMetAl 486	TGCTGAGAATGAGAAAAAAGGTCATCTGATTACA 1472	486 aPheSerLysAspHisGluGlnLeuTyrIleMetSerGluArgGlnLeuThrArgValPr 506	CACGCTTTATATGTGGCGTTCTCTAGCTGCATTATCCGCATCCC 1532	oValGluSerCysGlyGlnTyrGlnSerCysGlyGluCysLeuGlySerGlyAspPr 525	cercagnegericheagegrunalganicardnaaaagrenighanigeahenegaeee 1592	OHISCYSGIVTrpCysValleuHisAsnThrCysThrArg 538	-TTAAGCCAGGGATCCTGTAGA 1629
SAGCTCAATAGCATCCCTGGTTCT	GlnileAsnAspArgileLysGluArg gnarncaaaGGaCGGrryaAGGAACA-GAAAA	ArgGlyGluGlyThrLeuAspLew	 Gaagacaaagtgccaaagccaag	Ala-LeuLeuThrileAsp	::: TATAAAACCTCCATCGATTTCCC	JGlyValSerAspMetVa	 	gAspArgMetThrSerVal	GTACAGACTGACGGCCATCTCAGT	uAlaPheValGlyThrLysSerGl	CATCTTTGTTGGCTCTGAAGCTGG		CTCTTTGAACGACAGCGTATTACT	nAlaLeuGlnTyrGluThrValGl	: TGCTGAGAATGAGGAAGACAAAA	aPheSerLysAspHisGluGlnLe	GTTGGATAAAGATCACCACGCTTT	oValGluSerCysGlyGlnTyrGl	crcagregererage	OHisCysGlyTrpCysValLeuHi	GTATTGTGGCTGGTTAAGCCA
955	362 0		1074 (396	1134 7	413	1194 (429	1254 (445	1314 (459	1374	466	1434	486	1473	909	1533	525	1593
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yequence 12, Application US/09964956

yelblicarion No. US20040043926A1

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yelblicant Gerlach, Valerie L

yephlicant: Smithson, Glennda

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yephlicant: Bilerman, Karen

APPLICANT: Glosse, William M

APPLICANT: Glosse, William M

APPLICANT: Lepley, Demise M

APPLICANT: Grosse, William M

APPLICANT: Marshine E

APPLICANT: Marshine M

APPLICANT: Spitek, Kimberly A

APPLICANT: Spitek, Kimberly A

APPLICANT: Spitek, Kimberly A

APPLICANT: Shimkets, Richard A

ITTLE OF INVENTION: No. US20040043926A1e1 Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-124
  Sequence 12, Ar Sequence 19, Ar Sequence 30, Ar Sequence 31, Ar Sequence 31, Ar Sequence 31, Ar Sequence 350, A Sequence 173, A Sequence 173, A Sequence 91, Ap  Sequence 91, Ap Sequence 91, App Sequ
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13 US-09-964-956-12

15 US-10-451-010-19

15 US-10-175-523-95

13 US-10-087-684-31

14 US-10-087-684-31

15 US-10-087-684-31

16 US-10-087-684-31

17 US-10-087-684-31

18 US-10-24-824-31

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US-09-964-956-12
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
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-Q01/cgn2 1/USFTO_spool/US09964956/runat_19052004_160716_10957/app_query.fasta_1.2055
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-LOOPCL=0 -LOOPEXT=0 -UMITS=bits -START=1 -RND=-1 -MARRIX=blosum62
-TRANS=human40 -Cdi _LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-MAXIEN=200000000 -USER=US09964956 @CGN 1 1 353 @runat_19052004_160716_10957
-NCPIG= -IRCOPUS3 -NO WAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOÖX=100
-LONGLOG -DEV TIMEOÜT=120 -WAAN TIMEOUT=30 -THRRADS=1 -XGAPOPP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGĀPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                      May 23, 2004, 12:30:30; Search time 1094 Seconds (without alignments) 7876.420 Million cell updates/sec
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9990
1 MKAMPWNWTCLLSHLLMVGM.....QKLAYKLEQVITLMSLDSNK 1896
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| cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                           nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Kgapop 10.0 , Kgapext
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Description

us-09-964-956-13.rnpb

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       GACTACAAGGAGAAAAAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGCATCTGCAAAGCTG
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Mismatches:
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CURRENT APPLICATION NUMBER: US/09/964,956

PRIOR PEDICATION NUMBER: 60/25,631

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PLING DATE: 2000-09-28

PRIOR PAPLICATION NUMBER: 60/236,056

PRIOR PLING DATE: 2000-09-28

PRIOR PLING DATE: 2000-10-3

PRIOR PLING DATE: 2000-10-3

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-10-06

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2000-10-16

PRIOR PLING DATE: 2001-03-16

PRIOR PLING DATE: 2001-03-17

SEQ ID NO 12

PLENGTH PLING DATE: 2001-03-17

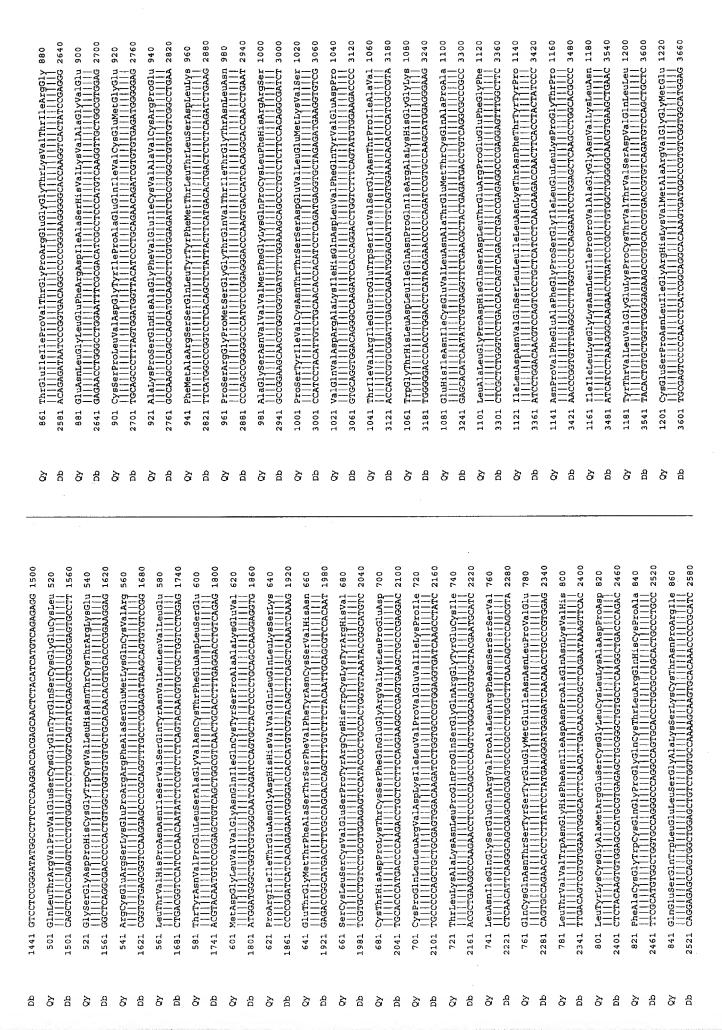
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PLENGTH PLING DATE: 2001-03-17

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PLENGTH PLING DATE: 2001-03-17

PRIOR PLING DATE: 2001-03-17
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CRGANISM: Homo sapiens
US-09-964-956-12
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Pred. No.:
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Matches:
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        APPLICANT WARREN, Bridget A. APPLICANT YUE, Henry
APPLICANT YUE, Henry
APPLICANT GIETZEN, Kimberly J. APPLICANT HONCHELL, Cynthia D. APPLICANT BURFORD, Neil
APPLICANT BURFORD, Neil
APPLICANT TANG, Y. Tom
APPLICANT TANG, Y. Tom
APPLICANT GANDHI, Amena R. APPLICANT GANDHI, Amena R. APPLICANT GANDHI, Richard C. APPLICANT BANDWAN, Olga
APPLICANT BANDWAN, Olga
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APPLICANT BANDWAN, Olga
APPLICANT BANDWAN, Olga
APPLICANT TANG, Monique G. APPLICANT TANG, WONIQUE G. APPLICANT TANG, MONIQUE G. APPLICANT TANG, MONIGER: US/10/451,010
CURRENT APPLICATION NUMBER: US 60/256,542
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR FILING DATE: 2001-12-2
PRIOR PILING DATE: 2001-05
NUMBER OF SEQ ID NOS: 20
SOFTHARE: PERL PROGRAM: G. SEQ ID NO 19
LENGTH: 6367
TYPE: DNA
ORGANISM: HOMO SADIENS
FRATURE: NAME/KEY: misc_feature
OTHER INFORMATION: 166

COTHER INFORMATION: a, t, c, g, or other
US-10-451-010-19
LU, Dyung Aina M.
WAREN, Bridget A.
YUE, Henry
GIETZEN, Kimberly J.
HONCHELL, Cynthia D.
BURFORD, Neil
BAUGHN, Mariah R.
TANG, Y. Tom
JACKSON Jennifer L.
GANDHI, Ameena R.
KALLICK, Deborah A.
BANDMAN, Olga
GRAUL, Richard C.
CHANLA, Narinder K.
LU, Yan
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                                                  121 AspTyrLysGluAsnArgLeuIleAlaCysGlySerLeuTyrGlnGlyIleCysLysLeu
                                                                                                                                                                  141 LeuArgleuGluAspleuPhelysleuGlyGluProTyrHislyslysGluHisTyrleu
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                                                                                                                       926 GACTACAAGGAGAACAAGGCTGATTGCCTGTGGGAGCCTGTACCAAGGATTCTGCAAGCTG
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ValGlnThrCysAsnGluProLeuThrThrThrAsnA
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Db 5186 CCTTGCTCCCACCGGCCCAAAGCTGCAGATCTGGAGTGGCGACAAGGAAGTGGGG Qy 1561 AlaArgMetIleLeuGlnAspGluAspIleThrThrLysIleGluAsnAspTrpLysArg	Qy 1621 TyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThrProMet Db 5426 TATGAAAACATGATCCGGTACACGGCAGCCCCGACAGCCTCCGCTCACGACACCTATG Qy 1641 IleThrProAspLeuGluSerGlyVallysMetTrpHisLeuValLysAsnHisGluHis Db 5486 ATCACTCCTGAACTGAAGTGAAGTCAAGATGTGACACTAGTGAAGAACACACAGAACACACAC	1661 5546 1681 5606	Oy 1701 SerThrAlaHiaArgGlySerAlaLeubroLeuAlaIleLysTyrMetPheAspPheLeu 5666 AGNA[4 W 4 1	DB 5846 AICCAIRAGAACAGCAICACAGACGCIGCCICTCTGTGGGTGGCTCAGACCTTCATGGACCTTCATGGACCTTCATGGACCTTCATGGACCTTCATGGACCTTCATGGACCTTCATGACTTCATGACTTCATGACTTGACAGACA	5966 1821 6026	Qy 1841 MerAsnGluPheAsnThrMetSerAlaLeuSerGluILePheSerTyrValGlyLysTyr	Db 6146 AGCGAGGAGATCCTTGGACCTCTGGACGACGACGACGAGGAGGAGAAACTGGCC Qy 1881 TYILYSLeuGluGlnValileThrLeuWetSerLeuAgpSer 1894	RESULT 3 US-10-175-523-95 ; Sequence 95, Application US/10175523
	1261 LysarglysSerargGluSeraspleuThrLeuLysargleuGluMetGluMetAspasn 1280 1261 LysarglysSerargGluSeraspleuThrLeuLysargleuGluMetGluMetAspasn 1280 1361 LysarglysSerargGluSeraspleuThrLeuLysargleuGluMetGluMetAspasn 1280 1346 AaaCGCAaGTCCCGCGCAAGTGACTCACGCTGAAGCGTGCAGTGCA	HisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrArgThrTyr 132	1341 ProGlyTyrArgGlnGluArgValGluLySGlyLeuLySLeuPheAlaGlnLeuIleAsn 1360	ArgaspargolyasnValalaSerLeuclaCorloanorricaAccoracoracoracoracoracoracoracoracoracor	4766 GCCACTGATGTGCTGAAGCTGCTGGCGGCCTCATTGACAGACCTGGAGGCAAG 4825 1421 AsnHisProLysbeuLeuLeuArgArgThrGluSerValAlaGluLysMetLeuThrAsn 1440	1441 TrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSer 1460	1481 AlaArgTyrSerLeuSerGluAspLysLeulleArgGlnGlnIleAspTyrLysThrLeu 1500		ProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgClnGlySerGly

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1570 AAGGGGCACAAGAACCACCACCCCCTAATGACTCTGCCCTCTGTGCCTTCCCCATC 1629
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                                                                                                                AlaSerMetIleLyslleProSerAspThrPheThrIleIleProAspPheAspIleTyr
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                                              AsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAspLysLeu
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Publication No. US20030096264A1
GENERAL INFORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Brock, David
APPLICANT: Lestek
APPLICANT: Alimczak, Leszek
APPLICANT: PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/10795-US3
CURRENT APPLICATION NUMBER: US 60/299,151
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR APPLICATION NUMBER: US 60/333,047
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2002-01-18
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Matches:
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| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)..(6730)
| CTHER INFORMATION: where n may
US-10-175-523-95
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Pred. No.:
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Leuarntyrthrvalleuvalglyglulysprocysthrvalthrvalserarpvalgin LeuLeuCysGluSerProAsnLeuIleGlyArgHisLysValMetAlaArgValGlyGly ThrProllelleLeuLysGlyLysAsnLeulleProProValAlaGlyGlyAsnValLys IlevalSerIleAlaValAlaGlyGlyLeuLeuIleIlePheIleValAlaValLeuIle |||||||||||:::||| |GGTGCTGGGAGCAGTGTAGCTGGGCAATCAGACCTGTGAATTCTATGGGAGG AspProThrileValArgileGluDroGluTrpSerileValSerGlyAsnThrProIle ProAlaLeuAlaLeuGlyProAspHisGlnSerAspLeuThrGluArgFroGluGluPhe MetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeuSerLeuProAla GlupheMetAlaArgSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeu 980 AsnalaglySerAsnValValValMetPheGlyLysGlnProCysLeuPheHisArgArg GlualaLysProSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgPro CATCTCTACAAGTGTGCAGCCCAGCGGGAAAGCTGTGGGTCTCTGCCTCAAGGCTGACCAC 3006 HisLeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAspPro lleThrGluileIleProValThrGlyProArgGluGlyGlyThrLysValThrIleArg AlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCygThrAsnProArg AspPheAlaCysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysPro

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                                                              CCCATGATCACCCCCAGACTTGGAGAGAGGGTGTCAAGGTTTGGCCATCTGGTGAAGAATCAT
                                                                                      GluHisGlyAspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLeu
                                                                                                GACCATGGTGACCAGAAGGAGGTGACCGGGGCAGCAAAATGGTGTCTGAGATCTACTTG
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                              ProMet11eThrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHis
  CCTAAGCAGACCTCCTCCTACAACATCCCTGCCTGCCAGCATCTCTCGGACATCCATT
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US-10-312-352-70

Sequence 70, Application US/10312352

Publication No. US20040053824A1

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.; TANG, Y: Tom

APPLICANT: YUE, Henry; AZIMZAI, Yalda

APPLICANT: HE, Ann; BATRA, Sajeev

APPLICANT: LO, Terence P.; NGOYEN, Danniel B.

APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.;

APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.;

APPLICANT: GENFORD, Neil; YAO, Monique G.;

APPLICANT: CRAMLA, Natinder K.; ELLIOT, Vicki S.;

APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
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AspileHisGluLeuThrSerAspLeuAspGlyAlaGlyIleProPheLeuAspTyrArg
                                                                                                         GACATCAATGAGCTAACCAGTGACTTGGATCGATCGGAATCCCTTACCTGGCTACCTGGCGT
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APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
APPLICANT: LU, Yan; BOROWSKY, Mark L.
APPLICANT: LU, Dyung Aina M.; RAMKUMAR, Jayalaxmi
APPLICANT: YANG, Junming, GTRTEAN, Klmberly J.
APPLICANT: YANG, Junming, GTRTEALM, Kajeopal
APPLICANT: WAREN, Bridget A.; GIETZEN, Klmberly J.
APPLICANT: WAREN, Bridget A.; GIETZEN, Klmberly J.
APPLICANT: DELEGEANE, Angel A.; THANGARZIU, Kavitha
APPLICANT: LE, Ernestine A.; THANGARZIU, Kavitha
APPLICANT: DELEGEANE, Angel A.; THANGARZIU, Kavitha
APPLICANT: DELEGEANE, ANGELLULAR MATRIX AND CELL ADHESION MOLECULES
TILE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
TILE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
THIR APPLICATION NUMBER: US 60/219,462
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/240,111
PRIOR APPLICATION NUMBER: US 60/240,116
PRIOR APPLICATION NUMBER: US 60/240,106
PRIOR PLING DATE: 2000-10-12
PRIOR PLING DATE: 2000-10-12
PRIOR PLING DATE: 2000-11-14
PRIOR PLING DATE: 2000-11-16
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) OTHER INFORMATION: Incyte ID No. US20040053824A1 7204554CB1
US-10-312-352-70
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ORGANISM: Homo sapiens
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                                       GluProTyrHisLysLysGluHisTyrLeuSerGlyValAsnGluSerGlySerValPhe
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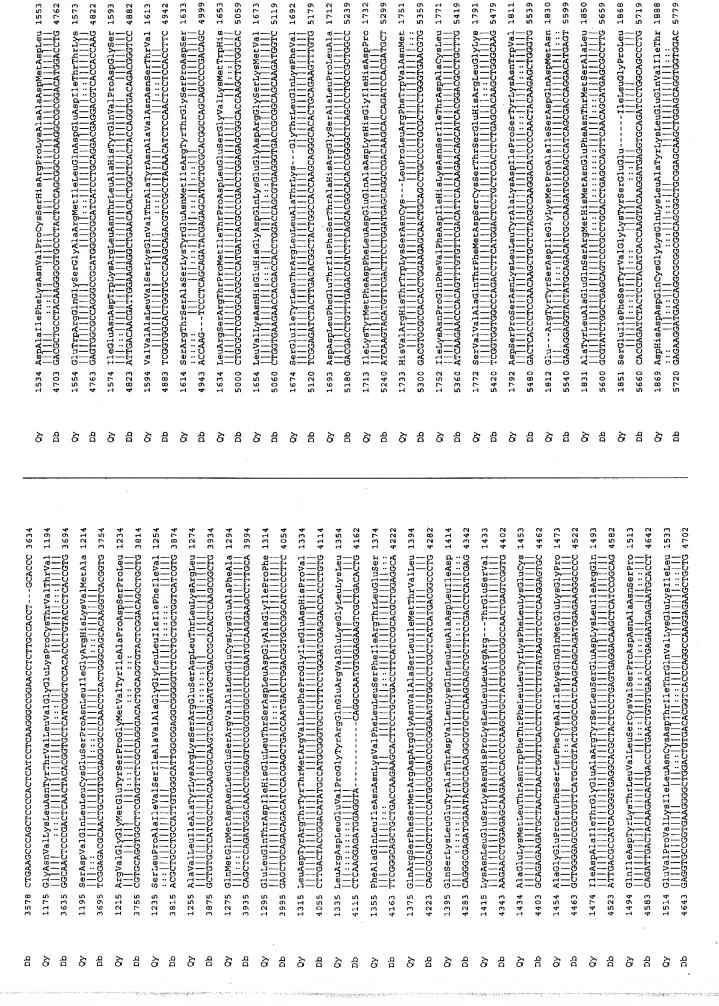
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APPLICANT: SILELMAN, AND STORE, WIlliam M. APPLICANT: Grosse, William M. APPLICANT: Grosse, William M. APPLICANT: Grosse, William M. APPLICANT: Rieger, Denied M. APPLICANT: Rieger, Denied M. APPLICANT: Rieger, Danied M. APPLICANT: Rieger, Danied M. APPLICANT: Graman, Stacie, J. APPLICANT: Graman, Stacie, J. APPLICANT: Buiger, Kimberly A. APPLICANT: Li, Li, APPLICANT: Beldgg, Perenc L. APPLICANT: Shenoy, Suresh G. APPLICANT: Shenoy, Suresh G. APPLICANT: Shenoy, Suresh G. APPLICANT: Shenoy, Velizar T. APPLICANT: Shenoy, Velizar T. APPLICANT: Corner, Corine A.M. APPLICANT: Malvanto, Pornet, Corine A.M. APPLICANT: Malvanto, Pornet, Corine A.M. APPLICANT: Malvanto, Bryan D. APPLICANT: Gangolii, Esha S. TITLE OF INTENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME PLICANT: Gangolii, Esha S. TITLE OF INTENTION: PROJECT CON-11-29
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR APPLICATION NUMBER: 60/250,926
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-06
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Conservative:
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Indels:
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (23)..(5797)
US-10-087-684-31
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Percent Similarity:
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Page 17

Db 170 AGGGCAGGGGTTCACAGCCCCCTTCCGCACCTTCTCGGCCAGCGCCTGGGGCC S1 PheAsnHisLeuValValAspGluArgThrGlyHislleTyrLeuGlyAlaValAspArg	8	Oy 71 IlefyrLysLesserSerAspLeuLysValLeuValThrHisGluThrGlyProAspGlu 90	Oy 91 ASPASNProLySCYSTYTProProArglleValGlnThrCysAsnGluProLeuThrThr 110	Oy 111 ThrAsnAsnValAsnLysMetLeuLeuIleAspTyrLysGluAsnArgLeuIleAlaCys 130	131 GlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuBheLysLeuGly 150	Qy 151 GlubroTyrHisLysGluHisTyrLeuSerGlyValAsnGluSerGlySerValPhe 170	Oy 171 GlyValIleValSerTyrSerAsnLeuAspAspLysLeuPheIleAlaThrAla 188	Qy 189 ValaspGlyLysProGluTyrPheProThrIeSerSerArgLysLeuThrLysAanSer 208 :::	Qy 209 GlualaaspGlyMetPhealaTyrValPheHisaspGluPheValAlaSerMetIleLys 228	Qy 229 IleProSerAspThrPheThrIleIleProAspPheAspIleTyrTyrValTyrGlyPhe 248	Qy 249 SerSerGlyAsnPheValTyrPheLeuThrLeuGlnProGluMetValSerPro 266	Qy 267 ProGlySerThrThrLysGluGlnValTyrThrSerLysLeuValArgLeuCysLysGlu 286	Qy 287 AspThrAlaPheAshSerTyrValGluValProlleGluVcysGluArgSerGlyValGlu 306	Qy 307 TyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeu 326	Qy 327 GlyValHisProAspAspAspAspLeuLeuPheThrValPheSerLysGlyGlnLysArgLys 346	Db 1061 GGCCTGAGGACGAGGACGTGCTGTTCACTGTGTCGCCCAGGGCCAGAAGAACGGC 1121	1061 GGCCTGAGACGAGGACGAGGACGTCTGTTCACTGTTTCGCCCAGGGCCAGAAGAACCGC 347 MetLysSerLeuAspGluSerAlaLeuCysIlePheIleLeuLysGlnIleAsnAspArg :::
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ACGATGGCCTGAGCAGC 5797	1	Sequence 31, Application US/10218779 Publication No. US20040029222A1 GENERAL INFORMATION: APPLICANT: Edinger, Shlomit	g, rg	Gerlach, Valerie Grosse, William Alsobrook II, John Lepley, Denise	Rieger, Daniel Burgess, Catherine Casman, Stacie Spytek, Kimberly	Boldog, Ferenc Li, Li Padigaru, Muralidhara Mishra, Vishnu	Patturajan, Meera Abnoy, Suresh Rastelli, Luca Tchernev, Velizar	Vernet, Corine Zerhusen, Bryan Malyankar, Uriel Guo, Xiaojia	ICANT: Miller, Charles ICANT: Gangolli, Beha B OF INVENTION Proteins and Nucleic Acids Encoding Same REFERENCE: 21402-214	CURRENT APPLICATION NUMBER: US/10/218,779 CURRENT FILING DATE: 2002-08-14 PRIOR APPLICATION NUMBER: 60/253,834 PRIOR FILING DATE: 2000-11-29	PRIOR APPLICATION NUMBER: 60/250,-926 PRIOR FILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: 60/264,180 PRIOR FILING DATE: 2001-01-25	APPLICATION NUMBER: 60/313,656 FILING DATE: 2001-08-20 APPLICATION NUMBER: 60/327,456 FILING DATE: 2001-10-05	SEQ ID NOS: 216 Patentin Ver. 2.1 1 895	TYPB: DNA ORGANISM: Homo sapiens 0-218-779-31		M. 28910500	62.74% Indels: 13.74% Gaps:

387 LysvallysAspileProCysSerSerAlaLeuLeuThrileAspAspAsnPheCysGly 406

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760 ValGlnCysGlnAsnThrSerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProVal 779 ::: :::	820 AspPheAlacysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysPro 839 2561 CGCTTCGAGTGCGATGCCGAGCCCGCTGCTCCCTGCGAACCACTGCGT 2620 840 AlaGlnGluSerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnPro 858	CTCAAGCTGTCCCCGAGACGGGC GUASSILeuGlyLeuGluPheArg GAGAACCTGGGCCTGCGATTCGAA ACSSEPFOLeuValAspGlyTyt ACSSEPFOLEUValAspGlyTyt FIGCGAGCCTGGGAGAGAGGGAGTA		958 AspLeuLysProSerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThr 977 :::	1016 GluMetLysValSerValGlnValAspArgAlaLysIleHisGlnAspLeuValPhe 1034 1161 AGCGCTCCCATCATCAACCGCGCCCCAGCTCAACCCTGAGGTGAAGTAC 3220 1035 GlnTyrValGluAspProThrileValArgIleGluProGluTrpSerIleValSerGly 1054 3221 AACTACACGAGGACCCCACCATCCTGAGGATCGAGCCATCAACAGGGGT 3280 1055 ABNThrProIleAlaValTrpGlyThrHisLeuAspLeuIleGlnAsnProGlnIleArg 1074 3281 GGGACCTCCTGACGGTCCACGCCAACCTGGCCACTGATCCGGATCGGG 3340 1075 AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet 1094 1075 AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet 1094 1095 ThrCysGlnAlaProAlaLeuAlaLeuAlaLeuGlyProAspHisGlnSerAcACACCACCATG 3397 1095 ThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHisGlnSerAcACACCACCATG 3397 1095 ThrCysGlnAlaProAlaLeuAlaLeuAlaLeuGlyProAspHisGlnSerAcACACACATG 3397 1095 ThrCysGlnAlaProAlaLeuAlaLeuAlaLeuGlyProAspHisGlnSerAcACACACATG 3397 1095 ThrCysGlnAlaProAlaLeuAlaLeuAlaLeuGlyProAspHisGlnSerAcACACACATG 3397 1095 ThrCysGlnAlaProAlaLeuAlaLeuAlaLeuAlaLeuGlyProAspHisGlnSerAcACACACATG 3397
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cgcgtgctgtttgtgggcaaaggcaatgggccacacgacaacggcatcatcgtgagcact
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CENTRALL INVEXTALLOW:
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature of INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature of INVENTION: Sets
TITLE OF INVENTION: Sets
TITLE REPRENCE: 689290-73
CURRENT APPLICATION NUMBER: US/69/236,033
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SOFTWARE: Patentin version 3.0
SEQ ID NO 313
LENDTH: 6252
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                                             SerGluilePheSerTyrValGlyLysTyrSerGluGlu-----IleLeuGlyProLeu
                                                                      US-09-964-956-13 (1-1896) x US-09-964-824A-313 (1-6252)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                        5780 ACGATGCCCTGAGCAGC 5797
                                                                                                                                                                                                                LeuMetSerLeuAspSer 1894
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2580.00
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Pred. No.:
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2372	TGCGTGTATGAGGCCCTGTGCAACACC 2398
852	LysSerLysCysThrAsnProArglleThrGluIlelleProValThrGlyProArgGlu 871
87	891
2459	 GGGGGCATCCGCATCCTGGGGTCCAATTTGGGCGTCCAAGCAGGGAACATC 2515
892	SerHisValLysValAlaGlyValGluCysSerProLeuValAspGlyTyrIleProAla 911
91	1 931
2576	SCGGAGACGCCTTTCACGGGGGGTG
932	IleCygValAlaValCysArgProGluPheMetAlaArgSerSer 946 :::
947	GlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArgGlyProMet 966
967	SerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySerAsnValVal 986
86	100
2792	CGGGTGACCTCAACGGCGTCCCGTGT 282
1007	AsnThrThrSerSerAspGluValLeuGluMetLysValSerValGlnValAspArgAla 1026
1027	Lysile
1035	
1055	AsnThrProlleAlaValTrpGlyThrHisLeuAspLeulleGlnAsnProGlnIleArg 1074
07	AlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMet 109
3059	:::
60	ThrCysGlnAla110
m d	CCGCGGGACGCTGAATCCCTGCAGCCCATGACGGTGGGTG
3155	AATGACACCAAGGCCTTCCTGTCCCCGGCTGTGCCTGAGGAGGCCGAGGCCTACAGG 321.
1120	Phe
3215	CTCACGGTGCTGATCGAGATGGACGGGCACCGTGCCCTTGCTCAC
1136	PheThrTyrTyrProAenProValPheGluAlaPheGlyProSerGlyIleLeuGluLeu 1155
1156	LysProG
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uLys :::	, AG	N A	tAlaar	CGAGTTCATTGTGAAGTT	oaspo 	CGACG	aValA	GGrer	sSerA	GAGCC	rArgV	GAGCG	uThrs	GACCA	gVall	CGTCT	uValF	CATC	eAsnA	GAACA	rMetA	_ 	uTyra	GTACT	rLys?	CAAG	rAsnī	CAACT	eSeri	CAAG	yGluz	GAAGG	rLeu	CCTG
alGlyGl	GGTGC	 ccggaggrgc	ValMetAl	TTCAT	AlaPr	GTGAG	Ileal	ATCGC	ArgLy	AGGAA	Gluse	GAGGA	GluLe	GACCA	MetAr	GACCG	LeuGl	CTGGA	LeuIl	CTGCT	Phese	TTCTC	LeuGl	CTGGP	Gluse	GTGGC	LeuTh	CTGTC	LeuPh	CTGT	ThrGl	CAGAR	Lystk	GCACC
3-	ĭ ā	8	, I	Ð	1	CACGG	alSer	TĊGTC	yrLys 	ACTGG	snLeu	GCCTG	leHis	TGGAG	YrThr	ACACC	rgAsp	GCAAG	lagln	CCAAC	rgSer 	GGGAG	erLye	GGAAA	snLeu	ACGTG	yaMet	GGATC	luPro	AGCCC	laile	CGGTA	17.Tq8:	AGTAC
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	o a	racrer	-	CACACACAAC	Tyril	GAGTA	ProAl	CCCAT	Leull	GTCTA	GlnMe	CAGCT	GlnTh	ATGAT	TyrAr	TACAA	Prova	ATGAT	Lysle	TACCA	Gluse	GAGAA	Valle	GCGCT	IleAs	CTGGA	ValAl 	GTGGT	CysAl	AGTGC	Proil	CCGGI	GlnGl	GATGA
	CAGGAGG GlnI.euI.	BACCTGTAC		CCACA	yGlyMetGluTyrSerProGlyMetValTyrIleAlaProAspSer :::	SCGTG		CGTG	aVal)	erAspLeuThrLeuLysArgLeuGlnMetGlnMetAspAsnL	AGTCC	aPheAlaGluLeuGlnThrAspIleHisGluLeuThrSe	ACCTG	GlyAlaGly1leProPheLeuAspTyrArgThrTyrThrMetArgValLeuPh	TGGAC	ProGly11eGluAspHisProValLeuArgAspLeuGluValProGl	AcGTG	ArgGlnGluArgValGluLysGlyLeuLysLeuPheAlaGlnLeuIleAsnAsnLy	CCCTC	hrLeu	CCCTG	ArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluTyrAlaT :::	CGGTG	AspValLeuLysGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGluSerLysAsnH	AGCTC	luser	AGACT	ThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSerLeuPh	AGGAC	alleLysGlnGlnMetGluLysGlyProlleAspAlalleThrGlyGluAl	AGGGC	LeuSerGludsplysleulledrgGlnGlnIleAspTyrLysThrLeuValle :::::	TGGGG
Val	SCTGC,	GAAGACGCTGACGGAGACCGAC		CAGAAACGAGACAC	0G1 y M6	3999		CTTGCCGCTGGTCAT	evalAl		JLeuG	BATCA	PAlaG.	CACAG	Phel	GTGC	eGluA	CAAGG	JLY8G	SCAGG	eArgT]	CCACA	IleM	GCTGA	aalaa :	CCTGG	gThrG	GTCTG	eLeuL	CCTCA	EG1uL	GGAAA	BLeuI	GCTGC
H	TGACG Peragn	CGGAC		AAACG/	SerPro	TGCT		CGCTC	Phelle		ysar	3AGAA(luCysLysGluAlaPhe	SAATT	[]ePro	ATCCC(31711	3GCGA(Jalgly	GTGGA	Phe II	TTCAT	SerLe	ICCCT	CeuLel	CTCTT	ArgAr	CGCAG	Lysph	CAGTA	31 nMe	CAGGT	Аврілу	ACGGG
euAsnTyı	CAAGGCGAT -Thrvalse	GCTG		GCAG	uTyre	ĠŦĠĠ		CTTG	elle	-	rreul	GTATC	rsGlu/	GAAGO	aGly		-Pro(GGACC	uArg	GGTGC	uSer	CAAT	lAla8	,cgcg	'sGlnl	CACG	ulen	GCTG	uTyr]	GTAC	rsGln(ACAT	erGlw	CGAC
1ьувье :	AACAA	AAGAC	1	, deceases	MetG]	cacar	rLeu	CTCAT	euLeuIl	1	LeuTh	CGAGA	CYBLY	TGCA	GlyAl	GAGGC	- 1	CTCCA	GlnG	CGGCC	LeuLe	CTCA	AsnVa	TACT	Leuly	ATGC/	Leule	CTGA	Leule	TGCC	IleLy	ATCA	rLeuSe:	CTC
Asnval	_ բ	CCAT	18L)	- KC	G1yG1y 	GCTCT	euSer	TCAGC	Ϋ́	1	erAsp	CCGAA	euG	GACCGC	euAsp(.gg		CTGCCC	TyrArg	Ę,	alPhe	CTTT	rgGly	AGGTC	spval	ACATO	roLys	CCAAC	hrPhe	CCATO	CysAla	AAGGCC	yrSer	r۱
76	62 A	22 A	10 H	482 C	17	542 Q	4 J	602 C	247 G	- 659	267 S	689 G	287 L	749 G	307 L	809 G	327 -	869 C	343 T	929 C	363 V	T 686	383 A	049 A	03	109 G	423 P	166 C	443 T	226 T	463 C	286 A	83 T	346 T
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1503	SerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeuAsnCys 1522
1523	ASPINIILETHIGINVALLYSGIULYSIIELEUASPAlailePheLysAsnValProCys 1542
1543	roLy: ::
1563	:: :: CAAC 4
1583	lnval
1603	rrg1
1623	9 ;
1643	etTrphisleuVallysaenHisGluHisGlyasp :: rgTGGCACCTGGTGCGGCCGACGACGAGGTGGAC
1663	GINLYSGIUGIYASPArgGIYSSr
1676	IleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspLeu 1695
1696	PheGluThrilePheSerThrAlaHigArgGlySerAlaLeuBroLeuAlaileLySTyr 17
1716	Met Phe Asp Phe Leuasp Gludinala Aspiyshis Glyilehis asp Prohis Valarg 1735
1736	HISTALTADIASSERABROSSLEUPROLEUARGPHETRPVALABRAMETILELYBABRARC 1755
1756	GINPhevalPheAspIleHisLyBASnSerIleThrAspAlaCySLeuSerValValAla 1775
1776	776 GINThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSer 1795
1796	ABNIVBLEULEUTYKALALIYSABDILEPKOSEKTYKLYBABNITFDVALGIUAKGTYKTYK 1815
1816 5279	SeraspileglyLysMetProalaileSeraspGlnaspMetAsnalaTyrLeuAlaGlu 1835
1836 5339	GINSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSer 1855
1856	TyrValGlyLysTyrSerGluGlulleLeuGlyProLeuAspHisAspAspGlnCysGly 1875

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrieuGlyAlaValAsnArgIleTyrLysLeuSerSerAspLeuLysValLeuValThr
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ThrieuLeuThrArgGlnProAlaProLeuSerGlnLysGlnArgSerPheValThrPhe
                                                                                                                                                                            Sequence 254, Application US/09930213
Sequence 254, Application US/09930213
Sequence 254, Application No. US20030170625A1
GENERAL INCORMATION:
APPLICANT: ROCENTHAL, ANNEE
APPLICANT: SCHEFE, REINHARD
APPLICANT: SCHEFE, ABRINDS
APPLICANT: THE NITSE, OLEG
APPLICANT: THE NITSE, OLEG
APPLICANT: THE SCHEFE, MARTIN
APPLICANT: HELLNEGEL, MARTIN
APPLICANT: SERSO GHRISTINE
TITLE OF INVENTION: DETECTION OF DIFFERENTIAL GENE EXPRESSIONS
FILE REFERENCE: ALBRE-14
CURRENT APPLICANT: 2001-01-31
PRIOR APPLICANT: 2001-01-31
PRIOR PLILING DATE: 2001-01-31
SPRIOR FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 885
SOFTWARE: Patentin Ver: 2.1
SEQ ID NOS: 82
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                                                              LysGlnLysLeuAlaTyrLysLeuGluGlnVal 1886
                                                                                       AAGATGCAGCTGCGCCTGCAGCAGCAGATT 5491
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US-09-930-213-254
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LENGTH: 6252
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                                                                ⋧
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LeuThrileAspAspAspPhe---CysGlyLeuAsp---MetAsnAlaProLeuGlyVal 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CysGlyGluCysLeuGlySerGlyAspProHisCysGlyTrpCysValLeuHisAsnThr 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACAGC-----CGGAGCAGTGGGGGCCCGGTGCGGCCTCTGCCTGCTTCCCGCTGGAC 961
181
                                                                                       201
                                                                                                                                                                                                                    665 ------GTGGCGGCCTTCGAGGACGGCCCCTACGTCTTCTTTGTCTTCACCAGCAG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 ArgleuCysLysGluAspThrAlaPheAsnSerTyrValGluValProIleGlyCysGlu 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 ArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaVal 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::
812 GACCCCGACATCCAC------GCCGCTGCCTTT-------GGCACCTGC 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSerLys 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 GlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIlePhelleLeuLys 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysiysileArgValAspGlyProArgGlyAsnAlaLeuGlnTyrGluThrValGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValAspProGlyProValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            496 IleMetSerGluArgGlnLeuThrArgValProValGluSerCysGlyGlnTyrGlnSer
                                                                                                                                                                                                                                                                              PheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPheAsp
                                                                                                                                                                                                                                                                                                                                                                          242 IleTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThrLeuGlnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnileAsnAspArgileLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 AspleuhlaTrpLeuLysVallys------AsplieProCysSerSerAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 SerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThrSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 GluMetValSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuVal
                                                                                                                               506 CGCGTGCTGTTGTGGGCAAAGGCAATGGGCCACACGACAACGGCATCATCGTGAGCACT
                                                                                                                                                                                    ArglysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGlu
162 GlyValAsnGluSerGlySerValPheGlyValIleValSerTyrSerAsnLeuAspAsp
                                          446 AGCAATGATGAGGGCGTGGCCACAGTGGGGCTGGTGAGCTCCACGGGTCCTGGTGGTGAC
                                                                                          LysLeuPhelleAlaThrAlaValAspGlyLysProGluTyrPheProThr1leSerSer
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1209 Db 3481 QY 1216 Db	3541 QY 1233 Db 3601		2y 1266 Db 3688	1286 QY 3748 Db	1306 Db	1326 UY 3868 Db	342 QY 928 Db	1362 QY 3988 Db	1382 QY 4048 Db	1402 QY 4108	422 QY	442 OY 225 Db	462 QY 285 Db	1482 QY 1482 Db 4345	1502 QY 4405 Db	1522 QY
Thrval Thrval SerAppaidinLeuLeuCysGluSerProAsnLeuIleGlyArg	cccaadgegegegegaaaacgagacaccacacacacgegegegege	LeuserLeu	G1u CAG	eraspleuThrleuLysArgleuGlnMetGlnMetaspasnLeuGluSerargValala :::::	LeuglucystysglualaphealagluLeuglnThraspileHisgluLeuThrSerAsp	LeuaspGlyalagly1leProPheLeuaspTyrargThrTyrThrMetargValLeuPhe :::	ProglyIleGluAspHisProValLeuArgAspLeuGluValProGly	TyrargGlnGluargValGluLysGlyLeuLysLeuPhealaGlnLeulleasnasnLys	ρ, υ	ArgGlyAsnValAlaSerLeuIleMetThrValLeuGlnSerLysLeuGluTyrAlaThr :::	spValLeulysGlnLeuLeuAlaAspLeuIleAspLysAsnLeuGluSerLysAsnHis ::::::	ProLysLeuLeuleuargargThrGluserValalaGluLysMetLeuThrasnTrpPhe :::	ThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeuPheSerLeuPhe :::	CysalaileLysGlnGlnMetGluLysGlyProileAspalaileThrGlyGluAlaArg	TyrserLeuserGluaspLysLeuIleargGlnGlnIleaspTyrLysThrLeuValLeu ::: :::: TaCaCTCTCaaCGACGCGGGGCTGCTGGGGGATGATGGGGGTGACGCACCCTGACGGTG	SerCysValSerProAspAsnAlaAsnSerProGluValProValLysIleLeuAsnCys
1191 ThrVal 3422 ACCATGAA(1210 HisLys	3482 CCCAAGCG 1217 GlyGlyMe 3542 GGCTCTCG	1234 LeuSerLeu 3602 CTCAGCCTC	1247 GlyLeuLe	1267 SerAsple::::::3689 GCCGAACG	1287 LeuGlucy 3749 GACCGCTG	1307 LeuAspGl::::3809 GTGCACGA	1327 3869 CTGCCCTC	1343 TyrArgGl :: 3929 CCGCGGCG	1363 ValPheLe 3989 TCTTTCCT	1383 ArgGlyAs ::: 4049 AAGGTCTA	1403 AspValLe :::: 4109 GACATCAT	1423 ProLysLe 4166 CCCAAGCT	1443 ThrPheleuL ::: 4226 TCCATCTGCC	1463 ·CysAlaIl 4286 AAGGCCAT	1483 TyrSerle	1503 SerCysVa

PheGluThrilePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyr MetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValArg GlnLysGluGlyAspArgGlySer------LysMetValSerGlu SerAsp11eGlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaGlu GlnSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheSer 4523 TCCTGCTGGCCCAGGCCAGACAGCGTGGTCCTGGAGTGGCGTCCGGGCTCCACAGCGCAG ---atcctgrcgaacctgacctgacgtcacagcggaaggccggtggaaggcggtcaac ThrieuAlaHisTyrGlnValProAspGlySerValValAlaLeuValSerLysGlnVal 1603 ThralaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSerLysTyrGlu GlnPheValPheAspIleHisLysAsnSerIleThrAspAlaCysLeuSerValValAla TyrvalGlyLysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGly 1563 MetileLeuGlnAspGluAspIleThrLysIleGluAsnAspTrpLysArgLeuAsn AsnMetlleArgTyrThrGlySerProAspSerLeuArgSerArgThrProMetlleThr SerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySerGlyAlaArg LysGlnLysLeuAlaTyrLysLeuGluGlnVal 1886

ठ JAPPLICANT: Hyeeq, Inc.

APPLICANT: Hyeeq, Inc.

APPLICANT: Tang, Y, Tom et al.

TILLE OF INVENTION: NO. US20040053245Alel Nucleic Acids and Polypeptides

TILLE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/10/276, 774

CURRENT PILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 09/496, 914

PRIOR PILING DATE: 2000-04-27

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PRIOR FILING DATE: 2000-02-03

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SEQ ID NOS: 2700

SEQ ID NOS: 2700

TYPE: NUMBER: 05/496, 914

PRIOR FILING DATE: TOWN OF SEQ ID NOS: 2700

SEQ ID NOS: 2700

SEQ ID NOS 388

LENGTHARE: CUSTOM

SEQ ID NOS 388

LENGTHARE: CUSTOM

SEQ ID NOS 388

CRANISM: Homo sapiens

US-10-276-774-838 632 652 343 716 262 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: SSULT 9 5-10-276-774-838/c Sequence 838, Application US/10276774 Publication No. US20040053245A1 GENERAL INFORMATION: 9.36e-265 2539.00 50.43% 33.05% Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores:

US-09-964-956-13 (1-1896) x US-10-276-774-838 (1-6329)

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rArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAspGl

5701	:
	uphevalalaserMetileLysileProSerAspThrPheThrileIleProAspPheAs 241
241	PhevalTyrPheLeuThrLeuGlnPr 261
5601	
261	oGluMetValSerProProGlySerThrThrLysGluGlnValTyrThrSerLysLeuVa 281 :::
281 5515	largleucyslysgluaspThralaPheasnSerTyrValGluValProlleGlyCysGl 301
301	uArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLysAlaGlyAlaVa 321
321	LeuGlyArgThrLeuGlyValHisProAspAspLeuLeuPheThrValPheSerLy 341
341	SGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysllePhelleLeuLy 361 :::
361	61 sGinileAsnAspArgileLysGluArgLeuGlnSerCysTyrArgGlyGluGlyThrLe 381
381 5251	uAspLeuAlaTrpLeuLysValLysAspIleProCysSerSerAlaLe 397 ::: GAAGGCCCGTGACATCTTCTACAAGCCCTTCCACGGCGATATCCAGTGCGGCGGCCACGC 5192
397	uLeuThrIleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeuGlyVa 415 ::: :: :::
415	ISETASPMETVALARGGLYILEProValPheThrGluAspArgAspArgMetThrSerVa 435
435	lile GACG
455	uLysLysIl : :: CCTCAAGGI
475 4954	lvalAspPr GGAGATAAA
495	
515	rcysglyglucysLeuglySerglyAspProHiscysglyTrpcysVallu:
535	
554	

AAGCAAGTCCTGCGTGGCCGTCACCAGCCCCAGAACATGAGCCGGGGGCCCA 4655 ITYRASNValLeuLeuValLeuGluThrTyrAsnValProGluLeuSerAlaG1 590	4 6 4 6 4 7 4 6	pcysprodinLeuLeuArgValAspLysileLeuValProValGluValileLysProil 720	Argcagdaatcrgcacctrrgcaccccaadgcrgcccacgargc 406LeuprovalGluLeuThrValValTrpasnGlyHisPheAsnIleAspAs 793	CAGCCTGTGCCGGGCCGCTAACCCCGACTACAGGTGTGCGTGGTGCGGGGGCCAGAGCAG 3896 CAGCCTGTACCAGGCCCTGTAACCCCGACTACAGGTGTGCGGGGGGCCAGAGCAG 3896 I CAGCGTGTATGAGGCCCTGTGCAACAC 3869 aLysSerLysCysThrAsnProArg11eThrGlu11eI1eProValThrGlyProArgG1 871
				· · · · ·
4174 4654 4654 650 4540 610	4492 649 4432 663 4372 683 683	700 4261 720 4201 740	100001	3955 831 3895 3868 871 3808 891

911	aGluGlnileValCyeGluMetGlyGluAlaLy8ProSerGlnHisAlaGlyPheValGl 931
931 3634	ulleCysValalaValCysArgProGluPheMetAlaArgSerSer 946
947 3592	-GInleuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysProSerArgGlyProMe 966
966 3535	tSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGlySerAsnValVa 986
986 3475	ValNetPheGlyLysGlnProCysLeuPheHisArgArgSerProSerTyrlleValCy 1006
1006	SASDTHRTHRSERSERASDGluValLeuGluMetLysValSerValGlnValAsDArgAl 1026
1026 3385	aLysile
1034 3325	eGInnyrvalGluAspProThrIleValArgIleGluProGluTrpSerIleValSerGl 1054
1054 3265	yasnThrProlleAlaValTrpGlyThrHisLeuAspLeuIleGlnAsnProGlnIleAr 1074
3207	gAlaLysHisGlyGlyLysGluHisIleAsnIleCysGluValLeuAsnAlaThrGluMe 1094 :::
1094	ThrCysGlnAlaProAlaLeuAlaLeuGlyProAspHis 1107 :::
3112	
3052	yPhelle
1135	nPheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLe 1155
1155 2955	uLysProGlyThrProllelleLeuLysGlyLysAsnLeulleProProValAlaGlyGl 1175
1175	yasnvaliysLeuasnTyrThrVal
1190	SThrvalThrvalSerAspValGlnLeuLeuCysGluSerProAsnLeuIleGlyAr 1209
1209	GHislysvalmetalaargva 1216

d d	1684	AGATCCTGTCGGACCTGACGTCACGCGGGAGGGCCGGTGGAAGCGTCA	1628
ò	1582	SnThrLeuAlaHisTyrGlnValProAspGlySerValValAlaLeuValSerLysGlnV	1602
QQ	1627	cttargcactacaardtccggarggagccacccrcarccrg	1581
ò	1602		1622
qq	1580	TCCAAGGTGGGGGTCTCCCAGCGGAGGACAGCCAGC	1541
ò	1622	leArgTyrThrGlySerProAspSerLeuArg	1642
ОЪ	1540		1512
8	1642	hrProAspLeuGluSerGlyValLysMetTrpHisLeuValLysAsnHisGluHisGlyA	1662
Dp	1511	CTGGAGGAGGAGAACCGGGTGTGGCACCTGGTGCGGCCGACGACGAGGTGG	1460
ò	1662	spGlnLysGluGlyAspArgGlySer	1675
QQ Q	1459	- ()	1400
λò	1675	IulleTyrLeuThrArgLeuLeuAlaThrLysGlyThrLeuGlnLysPheValAspAspL 	1695
Dp	1399	AGATCTACCTGACGCGGCTGCTCTCAGTCAAGGGCACACTGCAGCAGTTTGTGGACAACT	1340
δ	1695	euPheGluThrIlePheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysT	1715
QQ	1339	TCTTCCAGAGCGTGCTGGCGCCTGGGCACGCGGTGCCACCTGCAGTCAAGT	1289
ò	1715	yrMet PheAspPheLeuAspGluGlnAlaAspLysHisGlyIleHisAspProHisValA	1735
DP DP	1288	ACTICITCAGACITCCIGGACGACGAGGAGGACACAACAICCAGGAIGAAGACACCA	1229
ò	1735	rgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrpValAsnMetIleLysAsnP	1755
Db	1228	TCCACATCTGGAAGACGAACAGTTTACCGCTCCGGTTCTGGGTGAACATCCTCAAGAACC	1169
ò	1755	roglnPhevalPheAspIleHisLysAsnSerIleThrAspAlaCysLeuSerValValA	1775
QC	1168	CCACTTCATCTTTGACGTGCATGCACGTGGTGGACGCCTCGCTGTCATCATCG	1109
š	1775	aGlnThrPheMetAspSerCysSerThrSerGluHisArgLeuGlyLysAspSerProS	1795
Db	1108	cechearcticategatecctecacececaceacataaecteagccecatrccca	1049
'n	1795	erAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrT	1815
Db	1048	GCAACAAGCTGCTGTACGCCAAGGAGATCTCCACCTACAAGAAGATGGTGGAGGATTACT	689
ò	1815	yrSerAspIleGlyLysMetProAlaIleSerAspGlnAspMetAsnAlaTyrLeuAlaG	1835
Db	988	GGACATGAACACACACCTGGCA	929
Ολ	1835	luGlnSerArgMetHisMetAsnGluPheAsnThrMetSerAlaLeuSerGluIlePheS	1855
Db	928	Adatiticcedececacacacecerreaacacecereaacacacecerace	869
ζ	1855	erTyrValGlyLysTyrSerGluGlulleLeuGlyProLeuAspHisAspAspGlnCysG	1875
qq	868	aatacaccagaagtactatgacgagatcatcaatgccttggaggaggatcctgccgccc	608
ò	1875	lylysGlnLysLeuAlaTyrLysLeuGluGlnVal 1886	
qq	808	AGABATGCAGCTTCCGCCTGCAGCAGATT 774	
RESULT 10 US-10-240; Sequenc; Publica; GENERAL;	-425. e 35(ttion INF(RESULT 10 15-10-240-425-350 Sequence 350, Application US/10240425 Sequence 350, S20040033502A1 GENERAL INFORMATION APPLICANT: Williams, Amanda	

1684 AG---ATCCTGTCGGACCTGGACGTCACAGCGGGAGGCCGGTGGAAGCGCGTCA 1628

358 409 838 272 338 221 196 259 2 d b d d के नि के 원 상 원 8 6 8 6 8 8 8 8 8 요 요 셤 CysGlySerLeuTyrGlnGlyIleCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149 GCCGTGCGCTTCCCGCCCGCCGCCGCCGCCGAGCCGGTCACAGTGTTCCCCAGGATG 717 ------AspLysLeuPhelleAlaThrAlaValAspGlyLysProGluTyr 195 AspAsnProLysCysTyrProProArglleValGln---ThrCysAsnGluProLeuThr 109 GlyGluProTyrHisLysLysGluHisTyrLeuSerGlyValAsnGluSerGlySerVal 169 CTGAACGTGGCGGCCAACCCGAACGCGTCCACCGTGGGGCTAGTTCTGCCTCCCGCC 777 GCGGGCGCGGGGGCAGCCGCTCGTGGCGCCACGTACACCGGTTACGGCAGCTCC 837 ----- 357 AsnHisLeuValValAspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIle 71 TyrLysLeuSer---SerAspLeuLysValLeuValThrHisGluThrGlyProAspGlu 90 31 LeuLeuMetValGly------MetGlySerSerThrLeuLeuThrArgGlnProAla 32 ProLeuSerGlnLysGlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPhe APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Alvarez, Chris
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION Gene Expression Profiles in Esophageal Tissue FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT PILLOR DATE: 2001-03-09
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 350 TYPE: DNA CAGANISM: Homo sapiens FEATURE: OTHER INFORMATION: Genbank Accession No. US20040033502A1 AB014520 US-10-240-425-350 PheGlyVallleValSerTyrSerAsnLeuAsp------Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-964-956-13 (1-1896) x US-10-240-425-350 (1-6754) 346 CCCACGCCCACC-----8.88e-258 2475.50 48.64% 32.13% 24.78% Percent Similarity:
Best Local Similarity:
Query Match:
DB: 15 418 110 91 538 130 598 150 586 22 72 178 181 8 6 8 6 ò g ò d

::: 469 GCGAGCGCAAG-CTCAACATCCAGCTCAGCCAGAGCTGGACTGTGGAGCTGCTCAC 1527 449 GlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyProArgGlyAsnAlaLeu 468 ||| ||| ||| ||| 1030 CTGCACCCGTCC---GACCCGCCGGGTGCACAGTCCTACGGGTACCTGGCGCTCAAC 1086 378 GluGiyThrLeu------AspLeuAlaTrpLeuLysValLysAspIlePro 392 393 CysserSerAlaLeu-----LeuThrIleAspAspAsnPheCysGly---LeuAsp 408 MetAsnAlaProLeuGlyValSerAspMetValArgGlyIleProValPheThrGluAsp 428 240 285 LysGluAspThrAla-----------PheAsnSerTyrvalGluValPro 297 318 AlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThr 337 ValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIle 357 954 897 429 ArgAspArgMetThrSerValIleAlaTyrValTyrLysAsnHisSerLeuAlaPheVal Tretrecegegeaacegeagecregagaccacegerregagaacacecegagaregece 898 ATCCGCTCCCTGGACACGCGGCGACCTGGCCAAGCTCTTCACCTTCGACCTCAAA GlupheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPhe 1087 AGCGAGGCGCGCGGCGACAAGGAGAGCCCAGGCGCGGGAGCCTGCTGCTGCGCGCATCTGC 241 AspileTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThr---------LysGluGlnValTyrThrSerLysLeuValArgLeuCys PhelleLeulysGlnIleAsnAspArgileLysGluArgLeuGlnSerCysTyrArgGly 201 SerArgLysLeuThrLysAsnSerGluAlaAspGlyMetPheAlaTyrValPheHisAsp LeuGlnProGluMetValSerProProGlySerThrThr------469 GlnTyrGluThrValGlnValValAsp-----

Db 2827CC Cy 863 IleIleProValTP	2866 A	Qy 883 LeuGlyLeuGluPk Db 2926 CTGGGCCGGCGGCG	Qy 903 ProLeuValAspGl	Qy 923 ProSerGlnHisAl	3043	CY 943 AlaArgserserG ::: Db 3088 GGCAAGTCCCGGG	Oy 963 ArgGlyProMetSe : 		Db 3208 TCCGAGCTCCAGG	Qy 1002 SerTyrileValCy ::: Db 3268 ACCAGCATCGCCTC	1022	3322		3382	Db 3442 ACAGTGGCTGGTG	Cy 1079 GlyLysGluHisI	3502 GGCCGGGAGCCC-	1099	3559	Qy III3 GIYFNEITELEUM.::: Db 3619 GCAGACGAGGTGG	Qy 1133 LysThrAsnPheT	Db 3679 AGGTTCCGCCTGG	Qy 1153 LeuGluLeuLysP	Db 3739 ATCAAGCACCACO	Qy 1170 ProProValAlaG	0011	
500 ArgGlnLeuThrargValProValGluSerCysGlyGlnTyrGlnSerCysGlyGluCys 519 1795 CACCAGATGGCCAGGGTGGCGCCTGCAACGTGCACGCACTGTGGGGACTGC 1854	520 LeuGlyAspProHisCysGlyTrpCysValleuHisAsnThrCysThrArglys 539	0 GluargCysGluargSerLysGluProArgArgPheAlaSerGluMetLys	c descantistantictactorscancerificiosactas de descantación de la contracta de	1975 GGTGTCCTGCCATGÀCCGTCCTTCCGAGATCGATGTGCGCCÁGGAGTÀCCCAGGC 2034 576 LeuLeuValleuGluthrTvzasnValProGluLeuSeralaGlvValasnCvsThr 594	s argarectegagaretagagcagcetagcetagagagagagagagagagagagagagagagagagagag	595 PheGluAspLeuSerGluMetAspGlyLeuValValGlyAsnGlnIle 610	GlnCysTyrSerProAlaAlaLysGluValProArgllelleThrGluAsnGlyAspHis	5 GCCTACTGCAACCTCCTGCCGAGGGGACCAGTTTCCGCCCTTCCCCCCCAACCAA	031 ALBVALVALULHUEULHEULYBSELLINTGIYMECINTRREALASETINTSET 050 2215GTGACTGTTGAGATGTCTGTGAGGGTGAATGGGGGGGAACATCGTCAAGGCCAAT 2268	Phev	2269 TTCACCATCTACGACTGCACTGCACAGTGTACCCCCACACGCCTGTACCAGC 2328	665 CysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrHisAsp 684 2329 TGCTTGGGGAATGGCCTGTTTTTTTTGGAGACACACACAC	ProlysThrCysSerPheGlnGluGlyArgValLysLeuProGluAspCysProGlnLeu	2389 CAGTCTCGGTGCGAGGCCTCACCAAACCCCCACGAGCCCTCAGGACTGCCCCCGGACC 2445	LeuArgValAspLysIleLeuValProValGluValIleLysProIleThrLeuLysAla		725 LysAsnLeuProGinBroGinSerGlyGinArgGlyTyrCluCyslleLeuAsnlleGln 744 2506 GCCAACACTGCCTTTTTTCAGGGTGCAGCCCTGAGGGTGTAGATGTTTT 2550		-1	4 AsnThrSerTyrSerTyrGluGlyMetGlulleAsn		784 ValTrpAenGlyHisPheAsnileAspAenProAlaGlnAsniysValHisLeuTyriyys 903	n =	2725 TGTGCCATGGGCAGCCCCGACTGTTCCCAGTGCCTGGGCAGCCGGAAGACCTGGGTCACCTG 2784	823 CysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCysProAlaGlnGlu 842	2785 TGCATGTGGAGTGATGGCTGCCGCCTGCGGGGCCTCTGCAG 2826	843 SerGlnTrpLeuGluLeuSerGlyAlaLysSerLysCysThrAsnProArglleThrGlu 862
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ProglyThrProllelleLeu-----LysGlyLysAshLeulle 1169 ThrHisLeuAspLeuIleGlnAsnProGlnIleArgAlaLysHisGly 1078 ::: GCTGTGGCTGAGGGTACTGGACCCCGAGGAGGCACAGCGGGGCAGC 3678 GlyGlyAsnValLysLeuAsnTyrThrValLeuValGlyGluLysPro 1189 ValSerAspValGlnLeuLeuCysGluSerProAsn------ 1205 CyaksnThrThrSerSerAspGluValLeuGluMetLysValSerVal 1021 ValArgileGluProGluTrpSerileValSerGlyAsnThrProjle 1058 LeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPhe 1118 PheArgAspIleAlaSerHisvalLysvalAlaGlyvalGluCysSer 902 3087 3207 GAGCGTTTCCACATGGTGCAATGTGTCCATGGCCGTCCACATT 3501 /alMetPheGly---LysGlnProCysLeuPheHisArgArgSerPro 1001 |||::: stcttggtgaacgacacagacccttgcacgaagctgatgcgcacagat 3267 GlytyrileProAlaGluGlnileValCysGluMetGlyGluAlaLys 922 SerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAlaGly 982
:::|||||||||:::::||||||
GCCGGGGGCACCAGGATCACCATCCATGGAATGACCTCCATGTAGGC 3207 :::||| TCAGGTGTGGTGACCGTG------AACGCCTCTAAGGAG |||| :::||||::: ---GGGCTCCAGAGTCACGGGTCAGGTAGGCCAAGTAAGC ThrGlyProArgGluGlyGlyThrLysValThrlleArgGlyGluAsn AlagiyPheyajGluIleCysValAlaValCysArgProGluPheMet -----ABn AspAsnValGlnSerLeuLeulleLeu------

ValProcysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySer 1	1580 ArgleudsnThrLeudlaHisTyrGhnValProAspGlySerValValAlaLeu 1597	178 178	1668	AlaLeuProLeuAlaIIeLyBTyrMetPheAspPheLeuAspGluGlnAlaAspLysHis AAGCCCCCACTGGCTGTCAAGTACTTTTCGACTTCCTGGAGGAGCAGGCAG	TrpValAsnMetileLysAsnProclnPheValPheAspileHisLysAsnSerileTh TGGGTGAACATCTCGGGTTTTCTTTGGACAGACACACACA		1828 AspwetAsnAlaTyrLeuAlaGluGlnSerArgMetHisMetAsnGluPheAsnThrWet
8 8 8 8	8 8 8 8	8 8 8 8	8686	6 6 6	6666	8 & 8 &	8 6 8 8 8
3844 TGCCACATCCAGATTGTCTCTGACAGAATCATCCACTGGTCGGTC	s AladlyGlyLeuLeullellePheileValAlaValLeulleAlaTyrLygArgLygSer	1285 ValAlaLeuGluCysLysGluAlaPheAlaGluLeuGlnThrAspileHisGluLeuThr 1304 :::::::::::::::::::::::::::::::::::	ACCTTCTTCCCCAAGTGTTCCTCCCTTTATGAAGAGCGTTACGTGCTGCCCTCCCAGACC	4372 ATTCCTGAGAGCTGCCGGCCCAACATGGAAGAGGGAATTAGCTTGTCCTCACTACTC 4431 1360 ASDASDLygValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArgSerPheSer 1379	TyralarhraspvalleuLysGlnLeuLeuAlaAspLeulleAspLysAsnLeuGluSer 14	1440	GlualaargTyrSerLeuSerGluAspLysLeulleArgGlnGlnIleAspTyrLysThr 149 ::: :: :: ::

181 $\dot{\delta}$ 셤 ያ ያ 8 8 8 a Š g 8 8 8 ద ð 유 ò 임 ò g 8 셤 8 ò g 8 8 8 8 Sequence 729, Application US/10276774
| Publication No. US20040053245A1
| GENERAL INFORMATION:
| APPLICANT: Hyseq, Inc.
| APPLICANT: Tang, Y, Tom et al
| ITILE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
| FILE REFERENCE: 21272.030
| CURRENT APPLICATION NUMBER: US/10/276,774
| CURRENT APPLICATION NUMBER: 09/560,875
| PRIOR FILING DATE: 2000-04-27
| PRIOR FILING DATE: 2000-04-27
| PRIOR FILING DATE: 2000-04-27
| PRIOR FILING DATE: 2000-03
| NUMBER OF SEQ ID NOS: 2700
| SOFTWARE: Custom
| SEQ ID NO 729
| LENGTH: 7080 346 CCCACCCACC----- 357 91 AspAsnProlysCysTyrProProArgIleValGln---ThrCysAsnGluProLeuThr 109 110 ThrThrAsnAsnValAsnLysMetLeuLeulleAspTyrLysGluAsnArgLeulleAla 129 538 CTCACGGACAACTACAACAAGATCCTGCAGCCTGGACCCCGGCCTGGTAGTCGTG 597 130 CysGlySerLeuTyrGlnGly1leCysLysLeuLeuArgLeuGluAspLeuPheLysLeu 149 150 GlyGluProTyrHisLysLysGluHisTyrLeuSerGlyValAsnGluSerGlySerVal 169 658 GCCGTGCCGTTCCCCGCCCGCCGCCCCCCCGCCGACCCCGTCACGGTGTTCCCCAACATG 717 70 PheGlyValIleValSerTyrSerAsnLeuAsp------180 118 CIGAACGIGGGGGCAACCAACCAAACGCGICCACCGIGGGGCIAGIICIGCCICCGGC 777 358 AACAACTTCGCCCTGGACGCGGGCGGGGGACGTGTACCTGGGGGGCGCCGTCAACCGCTCT 417 72 TyrLysLeuSer --- SerAspLeuLysValLeuValThrHisGluThrGlyProAspGlu 90 15 LeuLeuMetValGly------MetGlySerSerThrLeuLeuThrArgGlnProAla 31 52 AsnHisLeuValValAspGluArgThrGlyHisIleTyrLeuGlyAlaValAsnArgIle 71 32 ProLeuSerGlnLysGlnArgSerPheValThrPheArgGlyGluProAlaGluGlyPhe 51 7080 652 332 747 304 60 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-964-956-13 (1-1896) x US-10-276-774-729 (1-7080) 2.99e-257 2471.00 48.43% 32.09% 24.73% 1888 ThrLeuMet 1890 5914 GCTTTGATG 5922 TYPE: DNA ORGANISM: Homo sapiens Percent Similarity: Best Local Similarity: Alignment Scores: US-10-276-774-729 Query Match: DB: Pred. No.: g d 유 Ωp Q, ò P ò à g ò a ò ò g 8 à δ

181	-AspLysLeuPheIleAlaThrAlaValAspGlyLysProGluTyr 19
778	GCGGGCGCGGGGAGCCGCCTGCTCGTGGGCGCCACGTACACCGGTTACGGCAGCTCC 837
196	PheProThrIleSer 200
201	SerArgLysLeuThrLysAsnSerGlualaAspGlyMetPheAlaTyrValPheHisAsp 220
O 1	luPheValAlaSerMetIleLysIleProSerAspThrPheThrIleIleProAspPhe 24
L)	
241	AspileTyrTyrValTyrGlyPheSerSerGlyAsnPheValTyrPheLeuThr 258 ::: :::::: ATCCTCAAGATCAAGGGGGGCCAAGGAGCAGCACAAGCTGGGCTTCGTGAGCGCCTTC 1029
259	LeuGlnProGluMetValSerProProGlySerThrThr
27	
1087	
285	LysGluAspThrAlaPheAsnSerTyrValGluValPro 297
1147	CTGCCCCACGCGCGGCGGCGACGCCAAGAAGCTCACCGAGTCCTACATCCAGTTGGGC 1206
298	IleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAlaTyrLeuSerLys 317
1207	1
318	AlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAspLeuLeuPheThr 337
6 6	ValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSerAlaLeuCysIle 357
ת	111CAACCGCCCCAGGGTCCCCGCGCCCCGCGCTGCTCCGGGCCGCACTCTGCGCCCCTGCACTCTGCGCCCCTGCGCGCGC
358	PhelleLeuLysGlnIleAsnAspArg1leLysGluArgLeuGlnSerCysTyrArgGly 377
37	uGlyThrieuAspieuAlaTrpLeulysVallysAspilePro 3
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393 1469	Cysserseralareu
40	co o
1528	Clecatericity and the control of the
4 00	GGTGGCCAGCGTCAACAACTACACAGCGGTCTTCCTG 16
449	GlyThrLysSerGlyLysLeuLysLysIleArgValAspGlyProArgGlyAsnAlaLeu 468
469	GlnTyrGluThrValGlnValValAsp
1681	
481	ValLeuArgAspMetAlaPheSerLysAspHisGluGlnLeuTyrIleMetSerGlu 499

1794 519 1854 1914 1914 1974 2034	4 9 0 9 0 4 0 9 4 9	2328 684 2388 2445 724 724 744 2505	763 2610 783 2664 803 2724 822 2784 842
	CTGTGAC IGINII CCGGATT CCGGATT YASPHIS GGACCAC TThrSer GGCCAAT	TACCAGC rHisAsp ::: TTCCAAC oGlnLeu cCGGACC uLySAla : GCCTCTG	Gln Gln Gln Gln Gln Gln Gln Gln
GTTACCTTTACCTGATGACGTCC InTyrGlnSerCysGlyGluCys TGCACTCCACCTGTGGGGACTGC euHisAsnThrCysThrArglys	-GlyvalAsnCysThr GGAGTGGCCTGTGAC 1ValGlyAsnGlnIle CTTGGTCACCAGTT rGluAsnGlyAspHis cCCCAACCAGGACCAC rPheAlaSerThrSer CATGGTCAAGGCCAAI	AGTGTACCCCCACACAGCCTGTACCAGC SLYSTYALGHISVALCYSTHTHISASD	aLeuArgPheAsnSerSerValGlnCysGln :::
Cadactcccctracctraccccccccccccccccccccccc	ralaGlyval GGCATGGAGATG CGCTGCTTTGGT CCTGCCTTTGGT CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCAAC CTTCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCCAAC CTTCCCCCCCAAC CTTCCCCCCCCAAC CTTCCCCCCCCAAC CTTCCCCCCCCAAC CTTCCCCCCCCCAAC CTTCCCCCCCCCAAC CTTCCCCCCCCCAAC CTTCCCCCCCCCAAC CTTCCCCCCCCCAAC CTTCCCCCCCCCCCCCAAC CTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	AGGGTACCCCCACACAGGCC SLYSTYLAEGHISVALCYS: [AGGCTAGCACTCCTGTTAGGCAGGCACTCCTGTAGGAGGACTGC] ILLYSLEUDTCGJUASCCYS AGGCTCCCAGGACTGC UVAILIELYSPROIJETHX: TGGCTCCCAGAACATCCTG GG]YTYTGJUCYSILELEU GGCCTGGAGTGTTTT	
INTYIGC INTYIGC IIII INCACTU INCAGAGA IASERG III INCAGTG INCAGTG INCAGTG INCAGTG	erala- drogca drogca hlyLeuV HlyLeuV CCCTG CCTTCC CCTTCC AGCGGA HlyMetT HlyMetT Horora	ACCCCC YrargH ::: AGCAGC euproG euproG lelysF ::: CCCAGA YrGluC	ersers Agrcrd snleus
GACTCCGC CYSG1YG1 IGCAACG1YG1 CYSValle IGTGCCC ArgPhea. ArgPhea. ArgPhea. ArgPhea. ArgPhea.	ulbeuse sccTcAc stAspG : ccAcAc rccAc rccAc rccAc rccAc rccAc	AAGTGT ABLYST SCAGCC ALLYSL LUVALI TGGGCT TGGLYT	heasns
AGCAGA usercy i:: i:: cccccc ccccccccccc cccccccccc		CTGCACAAGTGTA isTrpCysLysTy TCTGGTGCAGCCA 1yArgValLysLe ACCCCACGAGC roValGluValI1 CTACGGTGGCTC CTACGGGTGGCTC 1yGlnArgGlyTy CAGCCCT	aLeuArgPheAsnSerSerValdInc :::
AGTHGACCCAGCAGACTCCGGTTACCTG alprovalGluSerCysGlyGlnTyrGlnSerCys alprovalGluSerCysGlyGlnTyrGlnSerCys	uthrTytAsnValProGluLeuSerAlaGlyValAsnCy ::::::	CGACTGCAGCCGCACTGCACAAGTGTACCCCCACACACAC	roalal : AddCTG GGAAGA snIleA snIleA ::: CCCTGG erCYSG aCCTGTT
SCAGTT 3ValPr 3ValPr 3GTGAA PPOOL 11 CCCTA TTCCAG UThrVa GACCGT	uthrty ::: CTCGGG -GluAs CCGCAC OAlaAl UGlnLe UGlnLe TGAGAI	CTGCAG -:: GTGGCC rPheG] GGCCTC SIleLe GGCACC	gyalPr crrcca : rryrGl : Gaccc : Gaccc : Gaccc : Galus : Galus : Galus : Galus
CCATGTCATGAGTTTGACCCAGG ILEUThrArgValProValGluss :: GATGGCCAGGGTGAAGGTCGCCG YSerGlyAspProHiscysGlyT: TGCGGCGGACGCCTACTGCGGCT TGCGGCGGACGCCTACTGCGGCT CTGCACATTCAGCAGCAGC SVALARGLEUThrValHisPSCAGC GCTGCCATGACCTTCTGCCTTCT TCCTGCCATGACCGTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	UVALLEUGLUThrTyrAsnValProGluLeuSeralaGlyValAsnCysThr :::::::	CTACGA .:: .:: .:: .:: .:: .:: .:: .:: .:: .	uGlnar GGAGAT rTyrse ::::: GGCAGC aMetar aMetar GGGCAG
GTGCACCATGTCATGCATTTGACCCCAGCAGACTCCGGTTACCTTTACCTGATGACGCCCCCAGAGACTCCGGTTACCTTTACCTGATGACGCCCCCCCAGAGACTCCGGTTACCTTTACCTGATGACGCCCCCCCAGAGGACTCCCCTGAGACGTCCCCTGAGACGTCGCCAGGATGGCCAGGGTGACGCCCTGCACGTGCCAGGGTGAGGACGCCCTGCACGAGACGCCCAGGAGACGCCCTGCAGAGGGCCCAGCCGCCTGCAGAGGGCCCAGCCCTGCAGGGGGCCCCAGCGGGGCCCCTGCAGGGGGCCCCACCTGCAGGGGGCCCCAGCGGGACCCCAGGAGACGCGGGGCCCCAGCGGAACGCCCCCAGAGACCCCAGCCCCCAGCCCCCAGCCCCCC	ं के ल जिल्ला का की की जा की की	TTCACCCATCACGACTGCACACTGCACAGATGTACCCCCACACAGCCTGTACCAGG CysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisValCysThrHisAsp [::::::: TGCTGTCGGCACACTGCTTTCTGGTGCAGCCAGCACTCTGTTTTCAAG ProLysThrCysSerPheGlnGluGlyArgValLysLeuproGluAspCysProGluLeu CAGTCTCGGTGCAGCACACCCACCAGGACTGCCACAGGACTCCTAGGACC LeuargValAspLysIleLeuValProValGluValIleLysProIleThrLeuLysAla [:::	GlySerGluGlnArgValProAlaLeuArgPheAsnSerSerValGlnCysGln
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1735 500 1795 520 1855 540 1915 557	557 60 0 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	2269 665 2329 685 2389 705 746 725	25

2785 TGTATGTGGAGTGATGGC-----TGCCGCCTGCGGGGG-----CCTCTGCAG--- 2826

1181 PyThMYALINAYALINYARACCCAAATACCTCCAAATACTCTCCAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAATACAAAATACAAAATACAAAAATACAAAAAA	1511 AsnSerProGluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlu 1530 1511 AsnSerProGluValProValLysIleLeuAsnCysAspThrIleThrGlnValLysGlu 1530 1897 GGCATGGACGCTGAGCGGGCCATGGACACCGACACGCTGACAGGTCAAGGAG 4956	1531 LysileLeuaspalailePheLysasnValProCysSerHisArgProLysalaalaasp 1550	1551 MetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAspIle 1570	1571 ThrihriysileGluAsnAspTrpiysArgLeuAsnThrieuAlaHisTyrGlnValPro 1590 	1591 AspGlySerValValAlaLeuValSerLysGlnValThrAlaTyrAsnAlaVal 1608 ::: ::: ::	1609 ABnAsnSerThrValSerArgThrSerAlaSerLysTyrGluAsnMetIleArgTyrThr 1628 	1629 GlySerProAspSerLeuArgSerArgThrProWetlleThrProAspLeuGluSerGly 1648 ::::: 5200GACTTGGACACA 5211	1649 VallysMetTrpHisLeuVal	1659 GluHisGlyAspGluGlyAspArgGlySerLysMetValSerGluIleTyrLeu 1678	LysGlyThrLeuGlnLy 	1699 IlePheSerThralaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAsp 1718 	1719 PheLeudspGludlnAlaAspLysHisGlyIleHisAspProHisValArgHisThrTrp 1738	1739 LysSerAsnCysLeuProLeuArgPheTrpValAsnMetlleLysAsnProGlnPheVal 1758 :::	1759 PheAspIleHisLysAsnSerIleThrAspAlacysLeuSerValValAlaGlnThrPhe 1778	1779 MetapSerCysSerThrSerGluHisArgLeuGlyLysAspSerProSerAshLysLeu 1798 :::	1799 LeuTyrAlaLysAspIleProSerTyrLysAsnTrpValGluArgTyrTyrSerAspIle 1818 	1819 GlyLysWetProalalleSerAspGlnAspMetAsnalaTyrLeuAlaGluGlnSerArg 1838	1839 MethisMetAsnGluPheAsnThrMetSerAlabeuSerGluIlePheSerTyrValGly 1858 :::	LysTyrSerGluGluIleLeuGlyProLeuAspHisAspAspGlnCysGlyLysGlnLys
1181 PyrThrYalLeuWald)QuinyBroCyanhrYalThrYalSetAppWaldInGeuteu 1898 TACCGGGTAACANGCAAGTAGGTGGGGGGGGGGGGGGGGG	& &	& 8	8 &	ò a	& a	₩	ζς Q	ò 8	\$ g	& A	& A	· -	승 음	දි යි	충 a	SP 43	В 65	& A	<i>`</i> ∂
	TyrThrValLeuValGlyGluLy8FroCysThrValThrValSerAspValGlnLeuLeu 120	CysGluSerProAsn	ValGlyGlyMetGluTyrSerProGlyMetValTyrIleAlaProAspSerProLeuSer 123	LeubroAlaileValSerileAlaValAlaGlyGlyLeuLeuileIlePheileValAla 125 ACGGCCATARTCATCGTCATCTGAACGTCGAACGTGCTCATGTTGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	ValLeuileAlaTyrLysArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGln 127.	MetGlnMetAspAsnLeuGluSerArgValAlaLeuGluCysLysGluAlaPheAlaGlu 129	Comparation	LeuAspTyrArgThrTyrThrMetArgValLeuPhePro132	CIGGAGIAIRAGCACIICGIGACCCGCACCIICIICCCCCAAGIGIICCICCCTITATGAA 4	GAGCGTTACGTGCTGCCTCGCAGACCCTCAACTCCCAGGGCAGGTCCCCAGGGAA 43 AspHisProValleuArgAspLeuGluValProGlyTyrArgGlnGluargValGluLyB 13	GlybeuLysbeuPheAlaGlnLeuIleAsnAsnLysValPheLeuLeuSerPheIleArg 137	ThrheudluSerGinargSerPheSerMetArgAspArgGlyAsnValAlaSerLeuile 139	MetThrValLeuGlnSerLygLeuGluTyrAlaThrAspValLeuLysGlnLeuLeuAla 141	AsplealleAsplysAsnLeuGluSerLysAsnHisProlysLeuLeuLeuArgArgThr 143	GluServalAlaGluLysMetLeuThrAsnTrpPheThrPheLeuLeuTyrLysPheLeu 145 	Exercise Control Con	LysglyProlleAspAlalleThrGlyGluAlaArgTyrSerLeuserGluAspLyaleu 149 Lill	IleArgGlnGlnIleAspTyrLysThrLeuValLeuSerCysValSerProAspAsnAla 151	CTGCGGGAGAACATCGAGGCCAAGCCCCGGAACCTGAACGTGTCCTTCCAGGGCTGT

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TATGGGGAGCCCGTGCACCATGTCATGCAGCTTTGACCCAGCAGACTCCGGTTACCTTTAC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysThrArgLysGluArgCysGluArgSerLysGluProArgArgPheAlaSerGluMet 555
                                                                                                                                             294 ValGluValProIleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAla
:::||| |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   |||   
                                                                                                                                                                                                                                                                                                                                                                                                    TACATCCAC-------CGCCTGGTGTCGGTCTTCCCAGGGCCGGGAG
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                                                         ProSerAspThrPheThrIleIleFroAspPheAspIleTyrTyrValTyrGlyPheSer
||||||||||
                                                                                        ---dacaacarccrcaagarcaagcagggggggag
                                                                                                                        250 SerGlyAsnPheValTyrPheLeuThr-----LeuGlnProGluMetValSerProPro
AlaAspGlyMetPheAlaTyrValPheHisAspGluPheValAlaSerMetIleLysIle
                    CIGGCCAAGCTCTTCACCTTCGACCTCAAC------
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TATCAGCTGTCGGGCCCGAGCCCGAGCCGGGCCGTGGGCCCGTGGCCC
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639
317
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341
62
                                                                                                       RESULT 12
US-10-192-1943
US-10-08-192-1943
Sequence 1943, Application US/10087192
Sequence 1943, Application US/10087192
Sequence 1943, Application US/10087192
GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION UNMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR RILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 1943
LENGTH: 6340
TYPE: DNA
TYPE: DNA
COGANISM: Homo sapiens
US-10-087-192-1943
                                            US-09-964-956-13 (1-1896) x US-10-087-192-1943 (1-6340)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Score:
Percent Similarity:
Best Local Similarity:
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Query Match:
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e e		8	IleValCysGluMetGlyGluAla
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ð :		8 %	922 LysproSerGlnHisAlaGlyPheValGluIleCysValAlaValCysArgFroGluPhe 941
3 8		8 8	942 MetalaargSerSerGlnLeuTyrTyrPheMetThrLeuThrLeuSerAspLeuLysPro 961
음 장 음	1579 GGTCACCAGATTGCCTACTGCAACCTCCTGCGAGGGACCAGTTTCCGCCCTTCCCCCC 1638 627 ASnGlyAspHisHisValValGlnLeuGlnLeuLySSerLysGluThrGlyMetThrPhe 646	· &	SerArgGlyProMetSerGlyGlyThrGlnValThrIleThrGlyThrAsnLeuAsnAla
D Q		<u>අ</u>	ACCATGGGCCCCAAGGCCGGGGGCACCAGGATCACCATGGGGAATGACCTCCATGTA
کې و	647 AlaSerThrSerPheValPheTyrAsnCysSerValHisAsn 660	ž 8	982 GlySerAsnValValWatPheGlyLysGlnProCysLeuPheHisArgArgSer 1000
3 <i>3</i> 1	SerCysLeuSerCysValGluSerProTyrArgCysHisTrpCysLysTyrArgHisVal	8 8	1001 ProSerTyrileValCysAsnThrThrSerSerAspGluValLeuGluMetLysValSer 1020
8 &	1/33 GCCIGIACCAGCIGCCIGICGGCAAGIGGCCCIGITICIGGFGCAGCAGCAGCAGCACCC 1812 681 CysThrHisAspProLysThrCysSerPheGlnGluGlyArgValLysLeuProGluAsp 700	& £	1021 ValGlnValAppArgAlaLysIleHisGlnAspLeuValPheGlnTyrVal 1037
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<i>i</i> 6	ThrieulysAlalysAsnieuProGlnProGlnSerGlyGlnArgGlyTyrGluCysIle	<i>&</i> €	1053
3 &	1930 - 1961:General General IIII Chassaiche General General 1983 741 LeuksnileGingiySerdiuGinArgVal ProklaieukrgPheAsnSerSerSerVal 760	8	GlyThrHisLeuAspleulleGlnAspProGlnIleArgAlaLysHisGlyGlyLysGlu
qq	1984 TTTGGGCTGGAGGAGATCTTCGAGGCTGTGGGGTGAATGAGTCTGTTGTA 2034	8 &	110
<u>5</u> 55	761 GlnCysGlnAanThrSerTyrSerTyrGluGlyMetGluIleAsnAsnLeuProVal 779 :::	. අ	cccacgetergeaaggitereaactecaeceteateaetegeegee
<u>ئ</u> در	AlaGlnAsnLysVal	<i>ò</i> ₽	1102 AlaLeuGlyProAspHisGlnSerAspLeuThrGluArgProGluGluPheGlyPheIle 1121
3 &	HisbeuTyrLysCysGlyAlaMetArgGluSerCysGlyLeuCysLeuLysAlaAsp	ठे वि वि	1122 LeuAspAsnValGlnSerLeuLeuIleLeuAsnLysThrAsn 1135 :::
යි යි	2149 ATGGTCTATAACTGTGCCATGGGCAGCCCCGACTGTTCCCAGTGCCTGGGCGGGAAGAC 2208 819 ProAspPheAlaCysGlyTrpCysGlnGlyProGlyGlnCysThrLeuArgGlnHisCys 838	ò	PheThrTyrTyrProAsnProValPheGluAlaPheGlyProSerGlyIleLeuGluLeu
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8 8 7	ArgileThrGluileIleProValThrGlyProArgGluGlyGlyThrLysValThrIle	ò a	1170 ProProvalAlaGlyGlyAsnValLysLeuAsnTyrThrVal 1183
a &	2290 GAGATCCGCGCGATTGAGCCCCTGAGTGGCCCGTTGGACGGTGGGACCTGCTGACCATC 2349 879 ArgGlyGluAsnLeuGlybeuGluPheArgAspIleAlaSerHisValLysValAlaGly 898	8 8	1184 LeuValGlyGluLysProCysThrValThrValSerAspValGlnLeuLeuCysGluSer 1203 3382 AAGATAGGCQAGTAAGGTGGGAATGCGAGAATGTCTGAAGAGAATCATGACTGGTGG 3441
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204 Pr 442 GT	laargvalGlyGly 121: ::: TCCAGGTAGGGAAC 350	
1219 MetGl 3502 TTCAA	MetGluTyrSerProGlyMetValTyrileAlaProAspSerProLeuSerLeuProAla 1238 ::: TTCAACCAGACCATGCCACACTGCAGCTGGGGGGGGGGCAGCGAGACGGCCATC 3552	
1239 IleVa 3553 ATCGT		
1259 AlaTY :: 3610 GTCTT	AlaTyrLysArgLysSerArgGluSerAspLeuThrLeuLysArgLeuGlnWetGlnWet 1278 	
1279 AspAs ::: 3670 GAGGA	AspasnLeudluserargValAlaLeuGlu	
1289 3730 TCACG		
1304 Thrse 3790 ACCAA	ThrseraspleuaspGlyalaglyllebroPheLeuaspTyrargThrTyrThrWet 1322 ::: ::: ACCAAGGAGCTGAACCGCAGGGCATCCCCTTCCTGGAGTATAAGCACTTCGTGACC 3849	
1323 Argva. 3850 CGCAC	lleuPhePro cttcttccccaag	
1328 3910 ACCCT	1 8	
1339 GluVe ::::: 3970 AAGA	GluvalproglytyrarggingluargvalgluLysglyLeuLysLeuPhealaginLeu 1358 	
1359 IleAs 	IleasnAsnLysValPheLeuLeuSerPheIleArgThrLeuGluSerGlnArgSerPhe	
1379 SerMe	SerMetargaspargGlyasnValalaSerLeulleMetThrValLeuGlnSerLysLeu 1398 ::::: ::::: :: GCGGTGCGCACAGGTGCAGCTTGCTGACCATCGCGCTGCACGACAGGTG 4149	
1399 GluT) 4150 GAGT	GluTyralarhraspValLeuLysGlnLeuLeualaaspLeulleAspLysasnLeuGlu 1418 	
1419 SerLy ::: 4204 GCCG	ertysasnHisProLysLeuLeuLeuLagargThrGluSerValalaGluLysWetLeu 1438 ::	
1439 Thra. - 4264 ACCA	ThrasnTrpPheThrPheLeuLeuTyrLysPheLeuLysGluCysAlaGlyGluProLeu 1458 ACCAACTGGATGTCCATGTACAGCTGTCTGCGGGAGACGGTGGGGGAGCCATTC 4323	
1459 PheS	SerleupheCyshlaileLysGlnGlnWetGluLysGlyProlleAspalaileThr 1478 	
1479 G1yG : 4384 GGCA	GlyGlualaargTyrSerLeuSerGluaspLysLeuIleargGlnGlnIleaspTyrLys 1498 ::: ::: ::: ::: GGCAAGGCCGCTACACACTCAATGAGAGTGGCTGCTGCGGGAGAACATCGAGGCCAAG 4443	
1499 ThrL 4444 CCCO	ThrLeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLys 1518 	

1519	leuAspAlaIlePheLys 153 :: TGGAGGCCTTCTGCAAG 456
1539	9 ASNVA1ProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGly 1558
1559	9 SerglyalaargMetileLeuGlnaspGluaspIleThrThrLysIleGluasnaspTrp 1578
1579	9 LysargLeuasnThrLeualaHisTyrGlnValProAspGlySerValValala 1596
1597	597 LeuvalSerLygGlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThr 1616
161.	7 SerAlaSerLysTyrGluAsnMetlleArgTyrThrGlySerProAspSerLeuArgSer 1636
477	7 AAA 4779
163,	7 ArgThrProMet1leThrProAspLeuGluSerGlyValLySMetTrpHisLeuVal 1655
165	
481	6 CCIACGGACGAGCTGGCGGAGCCCAAGAAGTCTCACGGCAGAGCCATCGCAAG 4869
166	7 AspargGlySerLysMetValSerGlulleTyrLeuThrargLeuLeualaThrLysGly 168
168,	ThrLeuglnLysPheValAspAspLeuPhegluThrIlePheSerThrAlaHisArgGly 170
170	7 SeralaLeuProLeuAlaIleLysTyrMetPheAspPheLeuAspGluGlnAlaAspLys 1726
172	7 HisGlylleHisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArg 1746
174	
176	7 ThraspalacysLeuSerValValalaGlnThrPheMetAspSerCysSerThrSerGlu 1786
178	17 HisargleuGlyLysAspSerProSerAsnLysLeuLeuTyrAlalysAspIleProSer 1806 1816 1817 1818 1818 1819 1
180	1 0
182	7 GINASPMELASNATATYLLEUATAGUGINGSERARGMETHISMETASNGTUPheASNThr 184
184	7 MetSeralaleuSerGluilePheSerTyrValGlyLysTyrSerGluGluileLeuGly 186
186	7

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RESULT 14

US-10-276-774-773

US-10-276-774-773

Sequence 773, Application US/10276774

Publication No. US20040053245A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides

TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides

TITLE OF INVENTION: NO. US20040053245A1el Nucleic Acids and Polypeptides

CURRENT APPLICATION NUMBER: US/10/276,774

CURRENT FILING DATE: 2002-04-27

PRIOR PILING DATE: 2000-04-27

PRIOR PILING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: Custom

SEQ ID NO 773

LENGTH: 1088
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                                                                                                                                         1750 AsnMetileLysAsnProGlnPheValPheAsplleHisLysAsnSerileThrAspAla 1769
                                                                                                                                                                                                                                                        1790 GlylysAspSerProSerAsnLysLeuLeuTyrAlaLysAspIleProSerTyrLysAsn 1809
                                                                                                                                                                                                                                                                                                                                                                                            782 IGCCTCTCTGTGGTGGCTCAGACCTTCATGGACTCTTGCTCCACGTCAGAGCACCGGCTG 841
                                                                                  HisAspProHisValArgHisThrTrpLysSerAsnCysLeuProLeuArgPheTrpVal
                                                      602 ccccredccarcaagracargrrrgacrrccregargagcaggcraraaacarggcarr
                                                                                                      1770 CygleuSerValValAlaGlnThrPheMetAspSerCysSerThrSerGluHisArgLeu
                                                                                                                                                                                                                                                                            842 GGCAAGGACTCGCCCTCCAACAAGCTGCTGTATGCCAAGGACATCCCCCAGCTACAAGAAT
                                                                                                                                                                                                                                                                                                                                                                      1830 AsnalaTyrLeuAlaGluGlnSerArgMerHisMerAsnGluPheAsnThrMetSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                1022 CICTCAGAGATCTICTCCTATGTGGGCAATACAGCGAGGAGATCCTIGGACCTCTGGAC
AAGITIGIGGAIGACCICITIGAGACCAICITCAGCACGGCACACCGIGGCICIGCCCIG
                              1710 ProceutlaileLysTyrMetPheAspPheLeuAspGluGlnAlaAspLysHisGlyIle
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Matches:
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US-10-276-774-773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaAsnSerProGluValProValLys1leLeuAsnCysAspThr1leThrGlnValLys 1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1550 AspMetAspLeuGluTrpArgGlnGlySerGlyAlaArgMetIleLeuGlnAspGluAsp 1569
      5452 GCGCTGGAGGCCAACCCCAGGCCCGGAGGACACAACTGCAGCAAATTTGAGCAAGTG 5511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 AACTCCACGTCTCCAGGACCTCAGCAAGTAAATATGAAAACATGATCCGGTACACGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAAGATTCTGGATGCCATCTTCAAGAATGTGCCTTGCTCCCCACCGGCCCAAGCTGCA
                                                                                                                        ; Sequence 802, Application US/10108260A
; Publication No. US20040005560A1
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICAMT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; CURRENT APPLICATION NUBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOGTWARE: PatentIn Ver: 2.1
; SEQ ID NO 802
; LENGTH: 3666
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-108-260A-802
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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US-10-108-260A-802
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Pred. No.:
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1499 1560 GlyalaargMetileLeuGlnaspGluaspIleThrThrLysileGluasnAspTrpLys 1579 1580 ArgleuAsnThrleuAlaHisTyrGlnValProAspGlySerValValAlaLeuValSer 1599 1640 MetileThrProAspleuGluSerGlyValLysMetTrpHisLeuValLysAshHisGlu 1659 1679 1699 1719 1720 LeuaspGluGlnalaaspLysHisGlylleHisAspProHisValArgHisThrTrpLys 1739 LeuValLeuSerCysValSerProAspAsnAlaAsnSerProGluValProValLysIle 1519 LeuAsnCysAspThrIleThrGlnValLysGluLysIleLeuAspAlaIlePheLysAsn 1539 LysGlnValThrAlaTyrAsnAlaValAsnAsnSerThrValSerArgThrSerAlaSer 1619 1620 LysTyrGluAsnMetIleArgTyrThrGlySerProAspSerLeuArgSerArgThrPro 1639 1479 1540 ValProCysSerHisArgProLysAlaAlaAspMetAspLeuGluTrpArgGlnGlySer 1559 683 743 803 863 923 327 CTGGACTGTGACACGGGCACCCAGGCCAAGGAGAAGCTGCTGGACGCTGCCTACAAGGGC 386 506 507 AGGCTGAACACACACTGGCTCACTACCAGGTGACAGACGGGTCCTCGGTGGCACTGGTGCCC 566 146 206 266 86 624 AGATACGAGATGCTGCGCACGGCCAGCAGCCCCGACAGCTGCGCTCGCGCTCGCGCCCC 1660 HisGlyAspGlnLysGluGlyAspArgGlySerLysMetValSerGluIleTyrLeuThr 1700 PheSerThrAlaHisArgGlySerAlaLeuProLeuAlaIleLysTyrMetPheAspPhe 924 CIGGAIGAGCAGGCCGACAAGCACCAGAICCACGAIGCIGACGIGGGCCCACACCIGGAAG 87 AACTGGTTCACCTTCCTCTTGTATAAGTTCCTCAAGGAGGGGCTGGGGAGCCGCTGTTC 1480 GlualaargTyrSerLeuSerGluaspLysLeuIleargGlnGlnIleaspTyrLysThr GAGGCACGCTACTCCCCTGAGTGAGGACAAGCTCATTCGGCACCTGATTGACTACAAGACA 267 croaccercaacrororoaaccercagaaroaaaaroaaccercagosogo 1420 LysAsnHisProLysLeuLeuLeuArgArgThrGluSerValAlaGluLysMetLeuThr AAGAACCACCCCAAGCTGCTACTGCGCCGGACTGAGTCGGTGGCAGAGAAGATGCTAACT 1440 ASHTrpPheThrPheLeuLeuTyrIysPheLeuLysGluCysAlaGlyGluProLeuPhe SerieuPheCysAlaileLysGlnGlnMetGluLysGlyProlleAspAlaileThrGly 147 ATGCTGTACTGCGCCATCAAGCACCAGATGGAGAAGGGCCCCATTGACGCCATCACGGGT AspileHisLysAsnSerileThrAspAlaCysLeuServalval 1774 US-09-964-956-13 (1-1896) x US-10-276-774-773 (1-1088) 1460 207 1500 1520 1600 1740 27 dd Ор g à g $\dot{\delta}$ g 8 S 8 S ठ व ठ D ò G 8 8 8 원 ò ద ò ò d g ò g ò ò 8 à

APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Bater, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Eaton, Dan
APPLICANT: Goddard, Audrey
APPLICANT: Matable, Collin
APPLICANT: Matable, SERETED AND TRANSNEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ALIDE BNCODING THE SAME
FILE REPERRORE : PSG.0016-05-16
FILE REPERRORE : PSG.0016-05-16
FILE REPERRORE : PSG.0016-05-16
FILE REPERRORE : 1997-07-18
FILE REPERRORE : 1997-07-18
FILE REPERRORE : 1997-10-24
FRIOR FILING DATE: 1996-05-17
FRIOR PLILING DATE: 1996-05-17
FRIOR PLILING DATE: 1996-05-17
FRIOR PLILING DATE: 1996-06-18
FRIOR FILING DATE: 1996-06-18 214 PhealaTyrValPheHisAspGluPheValAlaSerMetIleLysIleProSerAspThr 2597 264 1 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-964-956-13 (1-1896) x US-10-245-752-91 (1-2597) 3,86e-138 1372.00 100.00% 99.62% 13.73% Sequence 91, Application US/102; Publication No. US20030064473A1; GENERAL INFORMATION: TYPE: DNA
CORGANISM: Homo Sapien
US-10-245-752-91 Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: 234 122 .. No.. a ਠੇ ò 셤 ð

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273	147	301	313	361	333	421	353	481	373	541	393	601	413	661	433	721	453	781		
4 ValTyrPheLeuThrLeuGlnProGluMetValSerProProGlySerThrThrLygGlu			4 ValGluValProlleGlyCysGluArgSerGlyValGluTyrArgLeuLeuGlnAlaAla	2 GTAGAGGTGCCCATTGGCTGTGGGCGCAGTGGGGGGGGGG	4 TyrLeuSerLysAlaGlyAlaValLeuGlyArgThrLeuGlyValHisProAspAspAsp	2 TACCTGTCCAAAGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCA	4 LeuLeuPheThrValPheSerLysGlyGlnLysArgLysMetLysSerLeuAspGluSer	2 CTGCTCTTCACCGTCTTCTCCAAGGCCCAGAAGCGGAAAATGAAATCCCTGGATGAGTCG	4 AlaLeuCysIlePheIleLeuLysGlnIleAsnAspArgIleLysGluArgLeuGlnSer	2 GCCCTGTGCATCTTCATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCT	4 CysTyrArgGlyGluGlyThrLeuAspLeuAlaTrpLeuLysValLysAsplleProCys	1 IGITACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	4 SerSerAlaLeuLhuThrIleAspAspAsnPheCysGlyLeuAspMetAsnAlaProLeu	2 AGCAGIGCGCICTIAACCAIIGACGAIAACIICIGIGGCCIGGACAIGAAIGCICCCCIG	4 GlyvalSerAspMetValArgGlyIleProValPheThrGluAspArgAspArgMetThr	2 GGAGTGTCCGACATGGTGCGTGGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACG	4 SerVallleAlaTyrValTyrLysAsnHisSerLeuAlaPheValGlyThrLysSerGly	2 TCTGTCATCGCATATGTCTACAAGAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGC	1 LysLeuLysLysIle 458	2 AAGCTGAAGAAGGTG 796
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